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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 23:41:33 / Search time 5120.53 seconds
(without alignments)
10809.568 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353

Sequence: 1 atgacacacagaccctca.....ggaccacagagcctcgtca 1353

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size: 30

Total number of hits satisfying chosen parameters: 1678

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1353 | 100.0 | 9842 | 6 AF005900 | AF005900 Homo sapi |
| 3 | 1251 | 92.5 | 2072 | 6 AR270618 | AR270618 Sequence |
| 4 | 1251 | 92.5 | 2072 | 6 HUMADRA2RA | M34041 Human alpha |
| 5 | 1251 | 92.5 | 3274 | 6 AX548756 | AX548756 Sequence |
| 6 | 902 | 66.7 | 1344 | 6 AX350490 | AX350490 Sequence |
| 7 | 902 | 66.7 | 1344 | 6 AF316895 | AF316895 Homo sapi |
| 8 | 902 | 66.7 | 22842 | 9 AC092603 | AC092603 Homo sapi |
| 9 | 819 | 60.5 | 885 | 9 HUMA2C2 | M38742 Human alpha |
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| 11 | 463 | 34.2 | 828 | 10 S67316 | S67316 alpha 2-adr |
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
Liggett, S.B. and Small, K.M.
Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 1 25-OCT-2001;
JOURNAL

Liaggett, Stephen B. (US) ; Small, Kersten M. (US)
Location/Qualifiers
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Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Homo sapiens alpha2b-adrenergic receptor (alpha2C2AR) gene,
DEFINITION complete cds.
ACCESSION AF005900
VERSION AF005900.1 GI:2245627
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 9642)
Cayla, C., Schack, S., Bouloumie, A., Devedjian, J.C. and Paris, H.
Alpha2C2-adrenergic receptor gene
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 9642)
Cayla, C., Schack, S., Bouloumie, A., Devedjian, J.C. and Paris, H.
Direct Submission
JOURNAL Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,
CHU Rangueil, Toulouse 31403, France
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LOCUS AX548756 3274 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 41 from Patent WO02061087.
ACCESSION AX548756
VERSION AX548756.1 GI:25813686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Burner, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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 LOCUS AX350490 Sequence 2 from Patent WO0179561.
 DEFINITION AX350490
 ACCESSION AX350490
 VERSION AX350490.1 GI:18616092
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 Liggett, S.B. and Small, K.M.
 AUTHORS Alpha-2 adrenergic receptor polymorphisms
 TITLE

JOURNAL Patent: WO 0179561-A 2 25-OCT-2001;
 Liggett, Stephen B. (US); Small, Kersten M. (US)
 FEATURES
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 Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 7
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DEFINITION cds: AF316895
VERSION AF316895.1 GI:12698669
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1344)
AUTHORS Small,K.M., Brown,K.M., Forbes,S.L. and Liggett,S.B.
TITLE Polymorphic deletion of three intracellular acidic residues of the
alpha 2B-adrenergic receptor decreases G protein-coupled receptor
kinase-mediated phosphorylation and desensitization
JOURNAL J. Biol. Chem. 276 (7), 4917-4922 (2001)
MEDLINE 21265012
PUBMED 11056163
REFERENCE 2 (bases 1 to 1344)
AUTHORS Small,K.M., Brown,K.M., Forbes,S.L. and Liggett,S.B.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Internal Medicine, University of
Cincinnati, 231 Bethesda Ave, Cincinnati, OH 45267, USA
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891 892
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGACCAACAGAGACCCCTACTCCGTGACAGCCAGGCAGCCATAGCGGCGCCATCACC 60
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QY 361 AACTCCAGCGCACCCCGCGCGCATCAAGTGCATATCTTCACTGTGTGCTCATCGCC 420
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DB 361 AACTCCAGCGCACCCCGCGCGCATCAAGTGCATATCTTCACTGTGTGCTCATCGCC 420
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DB 601 CGCAGCAACCGCAAGTGTCCAGAGGCGCAAGGCGGCGCTGGCAGGTATCCAGCGAG 660
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DB 841 GGCAGAGGCGCAAGAGAGGAGGTTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG 900
QY 901 GA 902
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RESULT 8
AC092603/c 22842 bp DNA linear PRI 01-MAR-2002
LOCUS Homo sapiens BAC clone RP11-139J6 from 2, complete sequence.
DEFINITION AC092603 AC073396
AC092603.2 GI:16303539
VERSION HTG.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
1 (bases 1 to 22842)
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Sulston, J.B. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792

REFERENCE
AUTHORS
TITLE
JOURNAL
2 (bases 1 to 22842)
Marinka, S., Abbott, A., Hawking, M., Elliott, G. and Doeber, A.
The sequence of Homo sapiens BAC clone RP11-139J6
Unpublished (2001)
3 (bases 1 to 22842)
Waterston, R.H.
Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 22842)
Waterston, R.H.
Direct Submission
Submitted (20-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 22842)
Waterston, R.H.
Direct Submission
Submitted (23-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 22842)
Waterston, R.
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916188.

REFERENCE
AUTHORS
TITLE
JOURNAL
Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@wustl.wustl.edu
Summary Statistics
Center project name: H_NH0139J06
Drafting Center: WIBR

COMMENT
NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPC1-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenken, E.,
Tateno, M., Caranese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.tegen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
the clone sequenced to the right is RP11-574017, 2000 bp overlap.
Actual end of this clone is at base position 48999 of RP11-574017.

Polymorphisms have been identified between AC013272 and AC092603.

The sequence of AC092603 has been incorporated into AC092603.

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| repeat_region | 1424..1449 /rpt_family="(GA)n" |
| repeat_region | 1495..1665 /rpt_family="Alu" |
| repeat_region | 1669..1966 /rpt_family="Alu" |
| repeat_region | 2812..2918 /rpt_family="MIR" |
| repeat_region | 3183..3448 /rpt_family="CT-rich" |
| repeat_region | 5541..5566 /rpt_family="AT-rich" |
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| repeat_region | 5873..6183 /rpt_family="Alu" |
| repeat_region | 6195..6301 /rpt_family="MIR" |
| repeat_region | 6627..6733 /rpt_family="L2" |
| repeat_region | 7278..7415 /rpt_family="MIR" |
| repeat_region | 7698..7723 /rpt_family="(GGCTG)n" |
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| repeat_region | 8863..8922 /rpt_family="MIR" |
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| repeat_region | 10172..10296 /rpt_family="MIR" |
| repeat_region | 10436..10550 /rpt_family="MIR" |
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| misc_feature | 12062..12257 /note="match to EST AA887330 (NID:G3002438) cJ40H05.61" |
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 15270 TTCTCATTTCTTTTACATCTTGGCAAGCTGTGATCTGTGCTGTGTTGACACAGC 15211
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DB 15030 GTGCACTGTGGCCATCAAGCCTGAGCCGCTACTGAGCCGCTGAGCCGCTGAGTAC 14971
QY 361 AACTCCAAAGCGACCCCGCGCGCGCATCAAGTGCATATCTCTCACTGTGTGCTCATGCC 420
DB 14970 AACTCCAAAGCGACCCCGCGCGCGCATCAAGTGCATATCTCTCACTGTGTGCTCATGCC 14911
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DB 14910 GCGGTATCTCGTGGCGGCGCTCATCTCAAGGGGAGCAAGGCGCGCGCGCGCGG 14851
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DB 14850 CGGCGCGAGTGAAGTCAACAGGAGGCTGTGATCATCTGTCCTCCAGCATCGGATCT 14791
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DB 14790 TTCTTGTCTCTTGGCTCATCATGATCTTGTCTACTGCGCATCTACCTGATTCGCCAA 14731
QY 601 CGGAGCAACCGAGAGTCCCAAGGCGCAAGGCGGCGCTGGCGAGGCTGATTCAGCAG 660
DB 14730 CGGAGCAACCGAGAGTCCCAAGGCGCAAGGCGGCGCTGGCGAGGCTGATTCAGCAG 14671
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DB 14670 CCCGACCGGACCATGCTGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14611
QY 721 GCTTCTGCGAGAGGTCAACGAGCACTGGAAGTCACTGGGAGAGAGAGAGGAGGAG 780
DB 14610 GCTTCTGCGAGAGGTCAACGAGCACTGGAAGTCACTGGGAGAGAGAGAGAGGAGG 14551
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QY 841 GGCAGGCGCAGAGAGAGGCTTTTGTGGGCGATCTCCAGAGATGAAGTGAAGAGAG 900
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DB 14430 GA 14429
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DEFINITION Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds.
ACCESSION M38742
VERSION M38742.1 GI:177867
KEYWORDS alpha-2 adrenergic receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 885)
AUTHORS Chang,A.C., Ho,T.F. and Chang,N.C.
TITLE In vitro amplification by polymerase chain reaction of a partial
gene encoding the third subtype of alpha-2 adrenergic receptor in
humans
JOURNAL Biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990)
MEDLINE 91054503
PUBMED 2173582
COMMENT Original source text: Human adult neuroblastoma DNA, clone PCR2.
Draft entry and computer-readable sequence for [Unpublished (1990)]
kindly submitted
by A.C.Chang, 20-SEP-1990.
Institute of Neuroscience
155, Sect II, Li-Moon St.
Taipei, Taiwan, 11221 ROC.
FEATURES
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| Oy | 921 | GAACCCCGAGGAGAGTCCAGTGTCTCCGGGCTCAGCTTCAGCCCCCGCTGCAGACGCA | 990 |
| Db | 148 | GAACCCCGAGGAGAGTCCAGTGTCTCCGGGCTCAGCTTCAGCCCCCGCTGCAGACGCA | 89 |
| Oy | 991 | CAGGCTCCCGGCTGCTGCGCACCCCTTAGTGCCAGAGTCTCTTGAGGAGGAGCGTGAGT | 10506 |
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| DEFINITION | alpha 2-adrenergic receptor [rats, Sprague-Dawley, islets of Langerhans, mRNA Partial, 828 nt]. | | |
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| VERSION | S67316.1 | GI:456949 | |
| KEYWORDS | Rattus sp. | | |
| SOURCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | |
| ORGANISM | 1 (bases 1 to 828) | | |
| REFERENCE | Wang,S.Y. and Pilkey,D.T. | | |
| AUTHORS | Identification in islets of Langerhans of a new rat alpha 2-adrenergic receptor | | |
| TITLE | Diabetes 43 (1), 127-136 (1994) | | |
| JOURNAL | Genbank staff at the National Library of Medicine created this entry [NCBI gisbed 140730] from the original journal article. | | |
| MEDLINE | 94085695 | | |
| PUBMED | 8262309 | | |
| REMARK | This sequence comes from fig. 1. | | |
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| Db | 22 | CTGTGCGGCATCAGCGCTGAGCCGCTACTCTAGGCGCGTGAAGCCGCGCTGAGTACAATCC | 81 |
| Oy | 367 | AAGGCAACCCCGCGCGCATCAAGTGCATCATCTGTGTGGCTCATGCGCGCGTC | 426 |

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| Db | 82 | AAGCCACCCCGCGCGCATCAAGTGCATCTCATCTGTGTGGCTCATTCGCGCGCTC | 141 |
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| Qy | 547 | GCTCGTGGCTCATATATATCTTGTCTACCTGGCGATCTACTGATTCGCCAAAGCAGC | 606 |
| Db | 262 | GCTCGTGGCTCATATATATCTTGTCTACCTGGCGATCTACTGATTCGCCAAAGCAGC | 321 |
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| Db | 322 | AACCCGAGAGGTCCCAAGGCGCAAGGGGGGCGCTGGGCAAGGTGAGTCCAAAGCAGCCCGA | 381 |
| Qy | 667 | CCCGACCATGTGTGGGGCTTTGGCTCTACGCAAACTGCAAGCCCTGGCTCTGTGTGCTTCT | 726 |
| Db | 382 | CCCGACCATGTGTGGGGCTTTGGCTCTACGCAAACTGCAAGCCCTGGCTCTGTGTGCTTCT | 441 |
| Qy | 727 | GCCAGAGAGGTCAAGGGAACCTCGAAGTCACTGGGGGAAGAGGAGGGGAGACCCCT | 786 |
| Db | 442 | GCCAGAGAGGTCAAGGGAACCTCGAAGTCACTGGGGGAAGAGGAGGGGAGACCCCT | 501 |
| Qy | 787 | GAAGATACTGGGACCCGGGCGCTTGGCAACCAGTTGGGCTGCCCTTCCCACTCAGGCGAG | 846 |
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| Qy | 847 | GGCCGAAAGAGAGGTGTTTGTGGGG | 871 |
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RESULT 12
LOCUS      567320      249 bp      mRNA      linear      ROD 26-FEB-1999
DEFINITION alpha 2-adrenergic receptor [rat, Sprague-Dawley, 22 month old
ACCESSION  S67320
VERSION    S67320.1  GI:456953
KEYWORDS
SOURCE
ORGANISM   Rattus sp.
            Rattus sp.
            Eutheria; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 249)
            Wang, S.Y. and Pilkey, D.T.
            Identification in blots of Langerhans of a new rat alpha
            2-adrenergic receptor
            Diabetes 43 (1), 127-136 (1994)
JOURNAL    94085695
MEDLINE    8262309
PUBMED
REMARK     GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsg 140734] from the original journal article.
            This sequence comes from Fig. 1.
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Best Local Similarity 100.0%; Pred. NO. 3.7e-106;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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| | | | | |
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| Oy | | 316 | ATCAGCCCTGACCGCCTTACTGGGCCGTGAAGCGCGCTGAGTAACAATCAAGCGACC | 375 |
| Dd | | 1 | ATCAGCCTGACCGCCTTACTGGGCCGTGAAGCGCGCTGAGTAACAATCAAGCGACC | 60 |
| Oy | | 376 | CCGGCGGCATCAAGTCATCATCTCTCACTGTGTGCTCATCGCCCGCTCATCTGCTG | 435 |
| Dd | | 61 | CCGGCGGCATCAAGTCATCATCTCTCACTGTGTGCTCATCGCCCGCTCATCTGCTG | 120 |
| Oy | | 436 | CCGGCCCCCTCATCTTCAAAGGCGCACCGAGGCCCCCAGCCCCGGGCGCCCACGTGCAAG | 495 |
| Dd | | 121 | CCGGCCCCCTCATCTTCAAAGGCGCACCGAGGCCCCCAGCCCCGGGCGCCCACGTGCAAG | 180 |
| Oy | | 496 | CTCAACCAAGAGGCGCTGGTATCATCTTGCGCTCCAGCATCGGATCTTTCTT | 545 |
| Dd | | 181 | CTCAACCAAGAGGCGCTGGTATCATCTTGCGCTCCAGCATCGGATCTTTCTT | 230 |
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| SC1315936 | | | | |
| DEFINITION | | | Sci1315936 | 1194 bp DNA linear MAM 22-MAY-2002 |
| ACCESSION | | | | |
| KEYWORDS | | | AJ315936 | Sorex cinereus partial adra2b gene for alpha 2B adrenergic receptor. |
| SOURCE | | | AJ315936.1 | GI:21212915 |
| ORGANISM | | | | adra2b gene; alpha 2B adrenergic receptor. Sorex cinereus (cinereus shrew) Sorex cinereus Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Insectivora; Soricidae; Soricinae; Sorex. |
| REFERENCE | | | | |
| AUTHORS | | | | 1 Murphy, W.J., Ezizirk, E., O'Brien, S.J., Maden, O., Scally, M., Donady, C.J., Teeling, E., Ryder, O.A., Stanhope, M.J., de Jong, W.W. and Springer, M.S. Resolution of the early placental mammal radiation using Bayesian phylogenetics Science 294 (5550), 2348-2351 (2001) |
| TITLE | | | | |
| JOURNAL | | | | |
| MEDLINE | | | | |
| PUBMED | | | | |
| REFERENCE | | | | |
| AUTHORS | | | | |
| TITLE | | | | |
| JOURNAL | | | | |
| FEATURES | | | | |
| source | | | | |
| gene | | | | |
| CDS | | | | |
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| Oy | 241 | CAGCGCAGCTGTGTGCAGAGGTGTACTCTGTGGCGCTGACGTCTCTTTCTGACCCTGTCATC | 300 |
| Db | 202 | CGGGCGCACCTGTGTGTGCAGGTGTACTGTGGCGCTCGACGTCTCTTTCTGTGACCTGTGCATC | 261 |
| Oy | 301 | GTGCACCTGTGGCGCATCAGCTCGGACCGGCTACTGGAC | 338 |
| Db | 262 | GTGCACCTGTGGCGCATCAGCTGTGGACCGGCTACTGGAC | 299 |

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| RESULT 14 | | | |
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| DEFINITION | Cynopterus sphinx partial aar2b gene for alpha adrenergic receptor 2B. | | |
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| VERSION | AJ251181.1 | GI:11322256 | |
| KEYWORDS | aar2b gene; alpha adrenergic receptor 2B. | | |
| SOURCE | Cynopterus sphinx (Indian short-nosed fruit bat) | | |
| ORGANISM | Cynopterus sphinx Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae; Pteropodinae; Cynopterus. | | |
| REFERENCE | 1 Madsen, O., Scally, M., Douady, C.J., Kao, D.J., Debry, R.W., Adkins, R., Amrine, H.M., Stanhope, M.J., de Jong, W.W. and Springer, M.S. Parallel adaptive radiations in two major clades of placental mammals Nature 409 (6820), 610-614 (2001) | | |
| JOURNAL MEDLINE | Nature | 409 (6820), 610-614 (2001) | |
| PUBMED | 21082081 | | |
| REFERENCE | 11214318 | | |
| AUTHORS | 2 (bases 1 to 1150) Madsen, O. Direct Submission Submitted (18-NOV-1999) Madsen O., Department of Biochemistry, University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen, NETHERLANDS | | |
| TITLE | Location/Qualifiers | | |
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| gene | | | |
| CDS | | | |
| BASE COUNT | 181 a 395 c 337 g 237 t | | |
| ORIGIN | | | |
| Query Match | 10.1%; Score 137; DB 4; Length 1150; | | |
| Best Local Similarity | 100.0%; Pred. No. 1.6e-56; | | |
| Matches 137, Conservative | 0; Mismatches 0; Indels 0; Gaps 0; | | |

| | | | |
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| Oy | 139 | CAGAACCGTTCCTGTGTGTGCTGTGGCGCGGCCGACGATCCTGTGTGGCCAGCCTCATCTC | 198 |
| Db | 101 | CAGAACCGTTCCTGTGTGTGCTGTGGCGCGGCCGACGATCCTGTGTGGCCAGCCTCATCTC | 160 |
| Oy | 199 | CTTTTCTGCTGTGCACAAGACAGCTGTGTGGCTACTTGTACTTCGCGCAGCTGTGTGCAG | 258 |
| Db | 161 | CTTTTCTGCTGTGCACAAGACAGCTGTGTGGCTACTTGTACTTCGCGCAGCTGTGTGCAG | 220 |

QY 259 GTGTACCTGGCGCTCGA 275
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 Db 221 GTGTACCTGGCGCTCGA 237

RESULT 15

S67317S2

LOCUS 246 bp mRNA linear ROD 26-FEB-1994
 DEFINITION alpha 2-adrenergic receptor (rats, Sprague-Dawley, 5 month old
 pancreas, mRNA Partial, 246 nt, segment 2 of 2).

ACCESSION

VERSION S67319.1 GI:456951
 KEYWORDS
 SEGMENT 2 of 2
 SOURCE Rattus sp.
 ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE

AUTHORS 1 (bases 1 to 246)
 TITLE Wang, S.Y. and Pilkey, D.T.
 Identification in islets of Langerhans of a new rat alpha
 2-adrenergic receptor

JOURNAL Diabetes 43 (1), 127-136 (1994)
 MEDLINE 94085695
 PUBMED 8262309

REMARK

Genbank staff at the National Library of Medicine created this
 entry [NCBI glibseq 140733] from the original journal article.
 This sequence comes from Fig. 1.

FEATURES

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1..246

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/mol_type="mRNA"

/db_xref="taxon:10118"

order(S67317.1:1..130:1..246)

/gene="alpha 2-adrenergic receptor"

BASE COUNT

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ORIGIN

Query Match

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 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 1006 CTGGCCACCTTACGTGGCCAGGTGCTCTGGGCGAGGGGCTATAGGTGGGAG 1065
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 Db 130 CTGGCCACCTTACGTGGCCAGGTGCTCTGGGCGAGGGGCTATAGGTGGGAG 189
 QY 1066 TGGTGGCGTCTGA 1077
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 Db 190 TGGTGGCGTCTGA 201

Search completed: February 8, 2004, 04:51:26
 Job time : 5127.53 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: February 8, 2004, 01:46:37 ; Search time 512.783 Seconds
(without alignments)
9654.769 Million cell updates/sec

Title: US-09-692-077D-2

Perfect score: 1344

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Gapop 60.0, Gapect 60.0

Searched: 2449703 seqs, 1841816367 residues

Word size: 30

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Published Applications NA:*

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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1 | 1344 | 100.0 | 1344 | US-10-001-073-2 | Sequence 2, Appl1 |
| 2 | 1191 | 88.6 | 1344 | US-09-825-923-1 | Sequence 1, Appl1 |
| 3 | 1191 | 88.6 | 1344 | US-10-077-870-1 | Sequence 1, Appl1 |
| 4 | 902 | 67.1 | 1353 | US-09-825-923-3 | Sequence 3, Appl1 |
| 5 | 902 | 67.1 | 1353 | US-10-077-870-3 | Sequence 1, Appl1 |
| 6 | 902 | 67.1 | 1353 | US-10-001-073-1 | Sequence 1, Appl1 |
| 7 | 902 | 67.1 | 1353 | US-10-001-073-1 | Sequence 1, Appl1 |
| 8 | 902 | 67.1 | 1353 | US-10-001-073-1 | Sequence 1, Appl1 |
| 9 | 65 | 4.8 | 60 | US-09-808-975-4948 | Sequence 4848, Ap |
| 10 | 65 | 4.8 | 60 | US-09-808-975-19227 | Sequence 19227, A |
| 11 | 45 | 3.3 | 1350 | US-10-001-073-24 | Sequence 24, Appl |
| 12 | 45 | 3.3 | 1350 | US-10-001-073-25 | Sequence 25, Appl |
| 13 | 45 | 3.3 | 1350 | US-10-001-073-25 | Sequence 25, Appl |
| 14 | 45 | 3.3 | 1350 | US-10-001-073-25 | Sequence 25, Appl |
| 15 | 39 | 2.9 | 463 | US-09-918-995-29557 | Sequence 29557, A |

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| 16 | 39 | 2.9 | 1382 | 12 | US-10-305-720-1256 | Sequence 1256, Ap |
| 17 | 39 | 2.9 | 1382 | 13 | US-10-101-510-754 | Sequence 754, App |
| 18 | 39 | 2.9 | 1382 | 13 | US-10-101-510-754 | Sequence 754, App |
| 19 | 34 | 2.5 | 1374 | 15 | US-10-001-073-42 | Sequence 42, Appl |
| 20 | 34 | 2.5 | 1386 | 15 | US-10-001-073-40 | Sequence 40, Appl |
| 21 | 34 | 2.5 | 2826 | 15 | US-10-225-567A-43 | Sequence 43, Appl |
| 22 | 33 | 2.5 | 6904 | 13 | US-10-311-455-48 | Sequence 48, Appl |

ALIGNMENTS

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| US-10-001-073-2 | | | | | | |
| Sequence 2, Application US/10001073 | | | | | | |
| Publication No. US20030113725A1 | | | | | | |
| GENERAL INFORMATION: | | | | | | |
| APPLICANT: Liggett, Stephen | | | | | | |
| TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms | | | | | | |
| FILE REFERENCE: 13073-PCT | | | | | | |
| CURRENT APPLICATION NUMBER: US/10/001,073 | | | | | | |
| CURRENT FILING DATE: 2001-11-01 | | | | | | |
| NUMBER OF SEQ ID NOS: 53 | | | | | | |
| SOFTWARE: PatentIn Ver. 2.0 | | | | | | |
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| Db | 61 | TTCTCTATTTCTTTACATCTTGGGACGCTGTGATCTCTGTGTTGACCAAC | 120 | | | |
| Qy | 121 | CGCTCGTGCGCCCTCGAAGCTGTGCTGTGCGTGGCGCGCGGCGGCTATCACC | 180 | | | |
| Db | 121 | CGCTCGTGCGCCCTCGAAGCTGTGCTGTGCGTGGCGCGCGGCGGCTATCACC | 180 | | | |
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 ; Publication No. US20030003470A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Salomon, Jukka T
 ; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
 ; FILE REFERENCE: 0933-0183P
 ; CURRENT APPLICATION NUMBER: US/10/077, 870
 ; PRIOR FILING DATE: 2002-05-21
 ; PRIOR APPLICATION NUMBER: FI 20010323
 ; PRIOR FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1344
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1341)
 ; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
 US-10-077-870-1

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| OY | 601 | CGAGCAACCGCAGAGGATCCAGAGGACCAAGAGGAGGAGCTGGGACAGGGTGTCCAAACAG | 660 |
| Db | 601 | CGAGCAACCGCAGAGGATCCAGAGGACCAAGAGGAGGAGCTGGGACAGGGTGTCCAAACAG | 660 |
| OY | 661 | CCCGACCCGACCATGTGTGGGCTTTTGGCTCAGACCACAACTGCCAGGCTTGAGCTCTGTG | 720 |
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| OY | 721 | GCTTCTGCGAGAGAGTTCACAGCACTCGAAGTCTCATCTGGGAGGAAGAGAGAGGGAG | 780 |
| Db | 721 | GCTTCTGCGAGAGAGTTCACAGCACTCGAAGTCTCATCTGGGAGGAAGAGAGAGGGAG | 780 |
| OY | 781 | ACCCCTGAAGAATCTGGGAGCCCGGAGCCTTGGCAACCGAGTTGGGCTGGCCCTTCCCACTCA | 840 |
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| Qy | 1141 | TGCTTCCCTCTCTTCTTCACTCAACAGCTTGGGCGCATCTGCGCGAAGCACTGCAAGTG | 1200 |
| Db | 1141 | TGCTTCCCTCTCTTCTTCACTCAACGCTTGGGCGCATCTGCGCGAAGCACTGCAAGTG | 1200 |
| Qy | 1201 | CCCCATGGCTCTTTCAGATTCTTCTTCTGATCGGCTACTGCAACAGCTCACTGAACCTT | 1260 |
| Db | 1201 | CCCCATGGCTCTTTCAGATTCTTCTTCTGATTCGGCTACTGCAACAGCTCACTGAACCTT | 1260 |
| Qy | 1261 | GTTATCTACACATCTTCAACACAGGACTTCGCGGTGACTTCCGAGGATCCTGTGCGCG | 1320 |
| Db | 1261 | GTTATCTACACATCTTCAACACAGGACTTCCGCGGTGACTTCCGAGGATCCTGTGCGCG | 1320 |
| Qy | 1321 | CCGTGAGACCGACAGCGGCTGTGTGA | 1344 |
| Db | 1321 | CCGTGAGACCGACAGCGGCTGTGTGA | 1344 |

RESULT 4
ITS-09-82

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Sequence 3 Application US/098259923
Patent No. US20010016338A1
GENERAL INFORMATION:
APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pasi
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Pesonen, Ullamari
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Jukka T
APPLICANT: Tuomala, Tomi-Pekka
APPLICANT: Lakka, Timo A
APPLICANT: Myllynen, Kristina
APPLICANT: Salonen, Riitta
APPLICANT: Kauppinen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIORITY APPLICATION NUMBER: 09/422,985
PRIORITY FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)-(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
US-09-825-923-3

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|---------------------------|--------|--------------|-------|--------------|
| Query Match | 67.1% | Score 902; | DB 9; | Length 1353; |
| Best Local Similarity | 100.0% | Pred. No. 0; | | |
| Matches 902; Conservative | 0; | Mismatches | 0; | Indels 0; |
| | | | | Gaps 0 |

Qy 1 TTGGACACACAGAGACCCCTACTCGTGGAGAGCCACAGCGGCATATGACGCGGCATACAC 60

Dd 1 ATGACACACAGAGACCCCTACTCGTGGAGAGCCACAGCGGCATATGACGCGGCATACAC 60

Qy 61 TTCTCATCTCTTTACCATCTTGAGCAACGCTCTGTATCCTGCTGTGTATGACAGC 120

Dd 61 TTCTCATCTCTTTACCATCTTGAGCAACGCTCTGTATCCTGCTGTGTATGACAGC 120

Qy 121 CGCTCGTGGCGGCCCTCAGAACCTGTTCCTGTGTGGCTTGGCGCGCGCGACATCCTGT 180

| | | | |
|----|-----|--|-----|
| Db | 121 | CGTGGCTGGGGCCCCCTCAGAACCTGTTCTCGGTGCTGGGCGGCCGCCGCAATCTG | 180 |
| OY | 181 | GTGGCACAAGCTCATCATCCCTTTTCTCGCTGGCCAAAGAGCTGCTGGCTCATCTGGTACTT | 240 |
| Db | 181 | GTGGCACAAGCTCATCATCCCTTTTCTCGCTGGCCAAAGAGCTGCTGGCTCATCTGGTACTT | 240 |
| OY | 241 | CGGCGCAGGTGGTGGAGAGGTGATCACTGGGCGCTCGAAGGTGCTTTCTGACCTGGTCAATC | 300 |
| Db | 241 | CGGCGCAGGTGGTGGAGAGGTGATCACTGGGCGCTCGAAGGTGCTTTCTGACCTGGTCAATC | 300 |
| OY | 301 | GTGCACTGTGGCCATCAGCCTGTGACCGCTTACTGGCCGTGAGCCGCGCTTGAATAC | 360 |
| Db | 301 | GTGCACTGTGGCCATCAGCCTGTGACCGCTTACTGGCCGTGAGCCGCGCTTGAATAC | 360 |
| OY | 361 | AATCTCAAGCGCAACCCCGCGCGCATCAAGTGCATCATCTCACTGTGTGGCTCATGCC | 420 |
| Db | 361 | AATCTCAAGCGCAACCCCGCGCGCATCAAGTGCATCATCTCACTGTGTGGCTCATGCC | 420 |
| OY | 421 | GGCGTATCGCTGGCGGCCCTCTATCAAAAGGCGCAACAGGGCCCCCAGCCGCGGG | 480 |
| Db | 421 | GGCGTATCGCTGGCGGCCCTCTATCAAAAGGCGCAACAGGGCCCCCAGCCGCGGG | 480 |
| OY | 481 | CGCCCCCAGTGCAGAGCTCAACAGGAGGCGTGTATCATCTGGCGCTCAGCATCGATCT | 540 |
| Db | 481 | CGCCCCCAGTGCAGAGCTCAACAGGAGGCGTGTATCATCTGGCGCTCAGCATCGATCT | 540 |
| OY | 541 | TTCTTTGCTTCCTGGCTCATCATGATCCTTGTCTTACTGGGCATCTTACTGATGCGCAA | 600 |
| Db | 541 | TTCTTTGCTTCCTGGCTCATCATGATCCTTGTCTTACTGGGCATCTTACTGATGCGCAA | 600 |
| OY | 601 | CGCAGCAACCGAGAAGTCCAGGGCCAAAGGGGGGGCGCTGGGCGAGGTGAGTCCAAAGCAG | 660 |
| Db | 601 | CGCAGCAACCGAGAAGTCCAGGGCCAAAGGGGGGGCGCTGGGCGAGGTGAGTCCAAAGCAG | 660 |
| OY | 661 | CCCCGACCCGACCATGTGGGGCTTTTGGCTCAGCCAAACCTGCCAGCCCTTGGCTCTGTG | 720 |
| Db | 661 | CCCCGACCCGACCATGTGGGGCTTTTGGCTCAGCCAAACCTGCCAGCCCTTGGCTCTGTG | 720 |
| OY | 721 | GCCTTCGCAGAGAAGTCAAGGACATCTCAAGTTCATCTGGGGAGAAAGAGAGGGGGAG | 780 |
| Db | 721 | GCCTTCGCAGAGAAGTCAAGGACATCTCAAGTTCATCTGGGGAGAAAGAGAGGGGGAG | 780 |
| OY | 781 | ACCCCTGAAGATTAAGTGGACCCGGGCTTGGCACCAGATTGGGCTGGCCTTCCCAATCA | 840 |
| Db | 781 | ACCCCTGAAGATTAAGTGGACCCGGGCTTGGCACCAGATTGGGCTGGCCTTCCCAATCA | 840 |
| OY | 841 | GGCGAAGGCGCAAGAGAGGATGTTTGTGGGGCATCTCCAGAGATGAAAGCTGAAGAGAG | 900 |
| Db | 841 | GGCGAAGGCGCAAGAGAGGATGTTTGTGGGGCATCTCCAGAGATGAAAGCTGAAGAGAG | 900 |
| OY | 901 | GA 902 | |
| Db | 901 | GA 902 | |

RESULT 5

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Sequence 3, Application US/10077870
Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salonen, Jukka T
TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens

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FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1350)
 OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
 US-10-077-870-3

Query Match 67.1%; Score 902; DB 15; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGACCAACGAGAGCCCTTACTCCGTGACAGGCGCCACAGCGGCATATAGGGGGCCATACAC 60
DB 1 ATGAGACCAACGAGAGCCCTTACTCCGTGACAGGCGCCACAGCGGCATATAGGGGGCCATACAC 60
QY 61 TTCCTCATCTCTTTACCATCTTGGGCAAGCTCTGGTCACTCGGGCTGTGTGACAGC 120
DB 61 TTCCTCATCTCTTTACCATCTTGGGCAAGCTCTGGTCACTCGGGCTGTGTGACAGC 120
QY 121 CGCTCGCTGCGCGCCCTCAGAAACCTGTTCTGTGTGCTGAGCGCGCGGCATCTG 180
DB 121 CGCTCGCTGCGCGCCCTCAGAAACCTGTTCTGTGTGCTGAGCGCGCGGCATCTG 180
QY 181 GTGGCCAGCTCATATCCCTTTTCCGTGCGCAACGAGCTGTGGCTACTGGTACTTC 240
DB 181 GTGGCCAGCTCATATCCCTTTTCCGTGCGCAACGAGCTGTGGCTACTGGTACTTC 240
QY 241 CGGCGACAGTGTGCGAGGTGTACCTGCGCTGAGCGTCTTCTGACCTGTGCATC 300
DB 241 CGGCGACAGTGTGCGAGGTGTACCTGCGCTGAGCGTCTTCTGACCTGTGCATC 300
QY 301 GTGCACTGTGCGGCATCAGCTGAGACCGGTAAGCGCGCGCGCTGAGATAC 360
DB 301 GTGCACTGTGCGGCATCAGCTGAGACCGGTAAGCGCGCGCGCTGAGATAC 360
QY 361 AACTCCAAAGGCAACCCCGCGCGCATGAGTCACTCTGATGTGCTATGCC 420
DB 361 AACTCCAAAGGCAACCCCGCGCGCATGAGTCACTCTGATGTGCTATGCC 420
QY 421 GCGGTATCTCGGTGCGCGCCCTCATATCAAGGGGCAAGAGGGCGCGCGCGGG 480
DB 421 GCGGTATCTCGGTGCGCGCCCTCATATCAAGGGGCAAGAGGGCGCGCGCGGG 480
QY 481 CGGCGCACTGTGCGGCATCAGCTGAGACCGGTAAGCGCGCGCGCTGAGATAC 540
DB 481 CGGCGCACTGTGCGGCATCAGCTGAGACCGGTAAGCGCGCGCGCTGAGATAC 540
QY 541 TTCCTCATCTCTTTACCATCTTGGGCAAGCTCTGGTCACTCGGGCTGTGTGACAGC 600
DB 541 TTCCTCATCTCTTTACCATCTTGGGCAAGCTCTGGTCACTCGGGCTGTGTGACAGC 600
QY 601 CGGAGCAACCGGAGGTCCCAAGGGGCGGCTGTGGGAGGTGAGTCCAGACAG 660
DB 601 CGGAGCAACCGGAGGTCCCAAGGGGCGGCTGTGGGAGGTGAGTCCAGACAG 660
QY 661 CGGAGCAACCGGAGGTCCCAAGGGGCGGCTGTGGGAGGTGAGTCCAGACAG 720
DB 661 CGGAGCAACCGGAGGTCCCAAGGGGCGGCTGTGGGAGGTGAGTCCAGACAG 720
QY 721 GCTTCTGCGAGAGGTCAACGAGCACTGCAAGTCTGAGGAGAGAGAGAGAGAG 780
DB 721 GCTTCTGCGAGAGGTCAACGAGCACTGCAAGTCTGAGGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAGAGATCTGGGAGCCCGGCTTGTGCAACCTGTTGGCTTCTCCACTCA 840
DB 781 ACCCTGAGAGATCTGGGAGCCCGGCTTGTGCAACCTGTTGGCTTCTCCACTCA 840
QY 841 GGCAGAGGCGAGAGAGGTGTTGTGAGGCACTCTCAGAGAGTGAAGTGAAGAGAG 900
DB 841 GGCAGAGGCGAGAGAGGTGTTGTGAGGCACTCTCAGAGAGTGAAGTGAAGAGAG 900
QY 901 GA 902
DB 901 GA 902
  
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RESULT 6

US-10-001-073-1
 Sequence 1, Application US/10001073
 Publication No. US20030113725A1
 GENERAL INFORMATION:
 APPLICANT: Liggett, Stephen
 APPLICANT: Small, Kirsten
 TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
 FILE REFERENCE: 13073-PCT
 CURRENT APPLICATION NUMBER: US/10/001.073
 CURRENT FILING DATE: 2001-11-01
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 1353
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-001-073-1

Query Match 67.1%; Score 902; DB 15; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAGACCAACGAGAGCCCTTACTCCGTGACAGGCGCCACAGCGGCATATAGGGGGCCATACAC 60
QY 61 TTCCTCATCTCTTTACCATCTTGGGCAAGCTCTGGTCACTCGGGCTGTGTGACAGC 120
DB 61 TTCCTCATCTCTTTACCATCTTGGGCAAGCTCTGGTCACTCGGGCTGTGTGACAGC 120
QY 121 CGCTCGCTGCGCGCCCTCAGAAACCTGTTCTGTGTGCTGAGCGCGCGGCATCTG 180
DB 121 CGCTCGCTGCGCGCCCTCAGAAACCTGTTCTGTGTGCTGAGCGCGCGGCATCTG 180
QY 181 GTGGCCAGCTCATATCCCTTTTCCGTGCGCAACGAGCTGTGGCTACTGGTACTTC 240
DB 181 GTGGCCAGCTCATATCCCTTTTCCGTGCGCAACGAGCTGTGGCTACTGGTACTTC 240
QY 241 CGGCGACAGTGTGCGAGGTGTACCTGCGCTGAGCGTCTTCTGACCTGTGCATC 300
DB 241 CGGCGACAGTGTGCGAGGTGTACCTGCGCTGAGCGTCTTCTGACCTGTGCATC 300
QY 301 GTGCACTGTGCGGCATCAGCTGAGACCGGTAAGCGCGCGCGCTGAGATAC 360
DB 301 GTGCACTGTGCGGCATCAGCTGAGACCGGTAAGCGCGCGCGCTGAGATAC 360
QY 361 AACTCCAAAGGCAACCCCGCGCGCATGAGTCACTCTGATGTGCTATGCC 420
DB 361 AACTCCAAAGGCAACCCCGCGCGCATGAGTCACTCTGATGTGCTATGCC 420
QY 421 GCGGTATCTCGGTGCGCGCCCTCATATCAAGGGGCAAGAGGGCGCGCGCGGG 480
DB 421 GCGGTATCTCGGTGCGCGCCCTCATATCAAGGGGCAAGAGGGCGCGCGCGGG 480
QY 481 CGGCGCACTGTGCGGCATCAGCTGAGACCGGTAAGCGCGCGCGCTGAGATAC 540
DB 481 CGGCGCACTGTGCGGCATCAGCTGAGACCGGTAAGCGCGCGCGCTGAGATAC 540
QY 541 TTCCTCATCTCTTTACCATCTTGGGCAAGCTCTGGTCACTCGGGCTGTGTGACAGC 600
DB 541 TTCCTCATCTCTTTACCATCTTGGGCAAGCTCTGGTCACTCGGGCTGTGTGACAGC 600
QY 601 CGGAGCAACCGGAGGTCCCAAGGGGCGGCTGTGGGAGGTGAGTCCAGACAG 660
DB 601 CGGAGCAACCGGAGGTCCCAAGGGGCGGCTGTGGGAGGTGAGTCCAGACAG 660
QY 661 CGGAGCAACCGGAGGTCCCAAGGGGCGGCTGTGGGAGGTGAGTCCAGACAG 720
DB 661 CGGAGCAACCGGAGGTCCCAAGGGGCGGCTGTGGGAGGTGAGTCCAGACAG 720
  
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QY 721 GCTTCTGACAGAGAGTCTAAAGCACTCTGAAATCTCTGGGGAAGAGAGAGAGGAG 780
DB 721 GCTTCTGACAGAGAGTCTAAAGCACTCTGAAATCTCTGGGGAAGAGAGAGAGGAG 780
QY 781 ACCCTGAAAGTACTGAGACCCGCGCTTGGCAACCCAGTTGGGCTGCTTCCCACTCA 840
DB 781 ACCCTGAAAGTACTGAGACCCGCGCTTGGCAACCCAGTTGGGCTGCTTCCCACTCA 840
QY 841 GGGCAGGGCCAGAGAGAGGAGTGTGTTGGGGCACTCTCAGAGATGAAGCTGAAGAGAG 900
DB 841 GGGCAGGGCCAGAGAGAGGAGTGTGTTGGGGCACTCTCAGAGATGAAGCTGAAGAGAG 900
QY 901 GA 902
DB 901 GA 902

RESULT 7

US-10-305-720-1181
Sequence 1181, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
FILE REFERENCE: Composition for the Detection of Signaling Pathway Gene Expression
CURRENT APPLICATION NUMBER: US/10/305,720
PRIOR FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1181
LENGTH: 2072
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181

Query Match 67.1%; Score 902; DB 12; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCAACAGAGACCCCTACTCCGCTGAGGCAAGGCGCATAGCGGCGCCATCACC 60
DB 413 ATGAGCAACAGAGACCCCTACTCCGCTGAGGCAAGGCGCATAGCGGCGCCATCACC 60
QY 61 TTCTCATTTCTTTTACCATCTTGGCAACGCTCTGTCATCTGCTGTGTGACGAC 120
DB 473 TTCTCATTTCTTTTACCATCTTGGCAACGCTCTGTCATCTGCTGTGTGACGAC 120
QY 121 CGCTGCG 180
DB 533 CGCTGCG 180
QY 181 GTGGCAAGCTCATATCTCTTCTGCTGGCAAGAGCTGCTGGCTGCTGCTGCTGCT 240
DB 593 GTGGCAAGCTCATATCTCTTCTGCTGGCAAGAGCTGCTGGCTGCTGCTGCTGCT 240
QY 241 CGGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 653 CGGGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 GTGCACTGTGCGCATCAGCTGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 713 GTGCACTGTGCGCATCAGCTGAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 AATCCCAAGGCAAGGCG 420
DB 773 AATCCCAAGGCAAGGCG 420
QY 421 GCGTCAATCTGCTGCG 480

DB 833 GCGTCAATCTGCTGCG 892
QY 481 CGCCCCAGTGAAGTCTCAACAGAGGCTGTGTAATCTGAGCTTCAGCATCGGATCT 540
DB 893 CGCCCCAGTGAAGTCTCAACAGAGGCTGTGTAATCTGAGCTTCAGCATCGGATCT 540
QY 541 TTCTTGTCTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 953 TTCTTGTCTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CGAGCAACCGCAGAGGCTCCAGGGCCAGAGGGGCGCTGGGAGAGAGAGAGAGAGAG 660
DB 1013 CGAGCAACCGCAGAGGCTCCAGGGCCAGAGGGGCGCTGGGAGAGAGAGAGAGAGAG 660
QY 661 CCGGACCGGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 1073 CCGGACCGGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GCTTCTGACAGAGAGTCAACGCACTGCAAGTCACTGGGAGAGAGAGAGAGAGAGAG 780
DB 1133 GCTTCTGACAGAGAGTCAACGCACTGCAAGTCACTGGGAGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAAAGTACTGAGACCCGCGCTTGGCAACCCAGTTGGGCTGCTTCCCACTCA 840
DB 1193 ACCCTGAAAGTACTGAGACCCGCGCTTGGCAACCCAGTTGGGCTGCTTCCCACTCA 840
QY 841 GGGCAGGGCCAGAGAGAGGAGTGTGTTGGGGCACTCTCAGAGATGAAGCTGAAGAGAG 900
DB 1253 GGGCAGGGCCAGAGAGAGGAGTGTGTTGGGGCACTCTCAGAGATGAAGCTGAAGAGAG 900
QY 901 GA 902
DB 1313 GA 1314

RESULT 8

US-10-225-567A-41
Sequence 41, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn P.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 3274
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match 67.1%; Score 902; DB 15; Length 3274;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAGCAACAGAGACCCCTACTCCGCTGAGGCAAGGCGCATAGCGGCGCCATCACC 60
QY 61 TTCTCATTTCTTTTACCATCTTGGCAACGCTCTGTCATCTGCTGTGTGACGAC 120
DB 61 TTCTCATTTCTTTTACCATCTTGGCAACGCTCTGTCATCTGCTGTGTGACGAC 120
QY 121 CGCTGCTGCG 180

GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1353 | 100.0 | 1353 | 15 | US-10-001-073-1 Sequence 1, Appli |
| 2 | 1302 | 96.2 | 1353 | 9 | US-09-825-923-3 Sequence 3, Appli |
| 3 | 1302 | 96.2 | 1353 | 15 | US-10-077-870-3 Sequence 3, Appli |
| 4 | 1251 | 92.5 | 2072 | 12 | US-10-305-720-1181 Sequence 1181, Ap |
| 5 | 1251 | 92.5 | 2072 | 12 | US-10-225-567A-41 Sequence 41, Appli |
| 6 | 918 | 67.8 | 1344 | 9 | US-09-825-923-1 Sequence 1, Appli |
| 7 | 918 | 67.8 | 1344 | 15 | US-10-077-870-1 Sequence 1, Appli |
| 8 | 902 | 66.7 | 1344 | 15 | US-10-001-073-2 Sequence 2, Appli |
| 9 | 60 | 4.8 | 65 | 13 | US-09-908-975-4848 Sequence 4848, Ap |
| 10 | 60 | 4.4 | 60 | 13 | US-09-908-975-18227 Sequence 18227, A |
| 11 | 45 | 3.3 | 1350 | 15 | US-10-001-073-24 Sequence 24, Appli |
| 12 | 45 | 3.3 | 1350 | 15 | US-10-001-073-25 Sequence 25, Appli |
| 13 | 45 | 3.3 | 3604 | 12 | US-10-305-720-1180 Sequence 1180, Ap |
| 14 | 45 | 3.3 | 3653 | 15 | US-10-225-567A-39 Sequence 39, Appli |
| 15 | 39 | 2.9 | 463 | 11 | US-09-918-995-29557 Sequence 29557, A |

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| 16 | 39 | 2.9 | 1382 | 12 | US-10-305-720-1256 Sequence 1256, Ap |
| 17 | 39 | 2.9 | 1382 | 13 | US-10-101-510-754 Sequence 754, App |
| 18 | 39 | 2.9 | 1758 | 13 | US-10-101-510-450 Sequence 450, App |
| 19 | 36 | 2.7 | 215980 | 11 | US-09-972-546-16 Sequence 16, Appli |
| 20 | 34 | 2.5 | 1374 | 15 | US-10-001-073-42 Sequence 42, Appli |
| 21 | 34 | 2.5 | 1386 | 15 | US-10-001-073-40 Sequence 40, Appli |
| 22 | 34 | 2.5 | 2826 | 15 | US-10-225-567A-43 Sequence 43, Appli |
| 23 | 33 | 2.4 | 6904 | 13 | US-10-311-455-48 Sequence 48, Appli |
| 24 | 32 | 2.4 | 5387 | 14 | US-10-001-873-22 Sequence 22, Appli |
| 25 | 32 | 2.4 | 5326 | 10 | US-09-818-264-3 Sequence 3, Appli |
| 26 | 30 | 2.2 | 171 | 9 | US-09-864-761-29686 Sequence 29686, A |
| 27 | 30 | 2.2 | 193 | 9 | US-09-864-761-23094 Sequence 23094, A |
| 28 | 30 | 2.2 | 311 | 9 | US-09-864-761-27934 Sequence 27934, A |
| 29 | 30 | 2.2 | 477 | 11 | US-09-918-995-27029 Sequence 27029, A |
| 30 | 30 | 2.2 | 485 | 9 | US-09-864-761-11354 Sequence 11354, A |
| 31 | 30 | 2.2 | 492 | 9 | US-09-864-761-6378 Sequence 6378, Ap |
| 32 | 30 | 2.2 | 506 | 9 | US-09-864-761-13125 Sequence 13125, A |
| 33 | 30 | 2.2 | 1922 | 15 | US-10-125-237-86 Sequence 86, Appli |
| 34 | 30 | 2.2 | 1922 | 15 | US-10-105-891-86 Sequence 86, Appli |
| 35 | 30 | 2.2 | 3069 | 13 | US-10-317-835-2 Sequence 2, Appli |
| 36 | 30 | 2.2 | 3254 | 13 | US-10-317-835-3 Sequence 3, Appli |
| 37 | 30 | 2.2 | 4242 | 13 | US-10-317-835-1 Sequence 1, Appli |
| 38 | 30 | 2.2 | 4571 | 13 | US-10-317-835-4 Sequence 4, Appli |
| 39 | 30 | 2.2 | 96599 | 12 | US-10-085-117-100 Sequence 100, App |

ALIGNMENTS

| | | |
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| RESULT 1 | US-10-001-073-1 | Application US/10001073 |
| 1 | Sequence 1, Appli | US/10001073 |
| 2 | Publication No. | US20030113725A1 |
| 3 | GENERAL INFORMATION: | |
| 4 | APPLICANT: | Liggett, Stephen |
| 5 | APPLICANT: | Small, Kirsten |
| 6 | TITLE OF INVENTION: | Alpha-2-adrenergic receptor polymorphisms |
| 7 | FILE REFERENCE: | 13073-BCT |
| 8 | CURRENT APPLICATION NUMBER: | US/10/001,073 |
| 9 | CURRENT FILING DATE: | 2001-11-01 |
| 10 | NUMBER OF SEQ ID NOS: | 53 |
| 11 | SOFTWARE: | PatentIn Ver. 2.0 |
| 12 | LENGTH: | 1353 |
| 13 | TYPE: | DNA |
| 14 | ORGANISM: | Homo sapiens |
| 15 | US-10-001-073-1 | |
| Query Match | 100.0% | Score 1353; DB 15; Length 1353; |
| Best Local Similarity | 100.0% | Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; |
| Matches 1353; | Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 | ATGAGCAACAGAGACCCCTACTCGTGCAGGACAGCGCCATAGCGGCGCATCACC 60 |
| DB | 1 | ATGAGCAACAGAGACCCCTACTCGTGCAGGACAGCGCCATAGCGGCGCATCACC 60 |
| QY | 61 | TTTCCTATTCTCTTACCATCTTGGCAACGCTGTGATATCTGAGCTGTGACCAAC 120 |
| DB | 61 | TTTCCTATTCTCTTACCATCTTGGCAACGCTGTGATATCTGAGCTGTGACCAAC 120 |
| QY | 121 | CGCTGCGCGGCGCCCTAGAACGTTCTGAGTGTGCGGCGCGCGCATATCCG 180 |
| DB | 121 | CGCTGCGCGGCGCCCTAGAACGTTCTGAGTGTGCGGCGCGCGCATATCCG 180 |
| QY | 181 | GTGGCAGCCTGATATCCCTTCTGCTGAGCAAGAGCTGAGGCTACTGATCTTC 240 |
| DB | 181 | GTGGCAGCCTGATATCCCTTCTGCTGAGCAAGAGCTGAGGCTACTGATCTTC 240 |
| QY | 241 | CGGCGCAGCTGATATCCCTTCTGCTGAGCAAGAGCTGAGGCTACTGATCTTC 240 |
| DB | 241 | CGGCGCAGCTGATATCCCTTCTGCTGAGCAAGAGCTGAGGCTACTGATCTTC 240 |
| QY | 301 | GTGGCAGCTGAGGCTGATATCCCTTCTGCTGAGCAAGAGCTGAGGCTACTGATCTTC 300 |
| DB | 301 | GTGGCAGCTGAGGCTGATATCCCTTCTGCTGAGCAAGAGCTGAGGCTACTGATCTTC 300 |

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DB 301 GTGACCTTGCGCCATGACCTGAGCCCTACTGGCCGTGAGCCGCGCCCTGAGATAC 360
QY 361 AACTCAAGGCGACCCCGCGCGCATCAAGTGCATCATCTCTCATCTGTGTGCTCATGCCC 420
DB 361 AACTCAAGGCGACCCCGCGCGCATCAAGTGCATCATCTCTCATCTGTGTGCTCATGCCC 420
QY 421 GCGGTATCTGCTGCGCGCCCTCATCTCAAGGCGGACCAAGGCGCCGCGCGCGG 480
DB 421 GCGGTATCTGCTGCGCGCCCTCATCTCAAGGCGGACCAAGGCGCCGCGCGCGG 480
QY 481 GCGGTATCTGCTGCGCGCCCTCATCTCAAGGCGGACCAAGGCGCCGCGCGCGG 540
DB 481 GCGGTATCTGCTGCGCGCCCTCATCTCAAGGCGGACCAAGGCGCCGCGCGCGG 540
QY 541 TTCTTTGCTCTGCTGCTCATCATCATCTCTGTGTCTACTCTGCGCATCTCAAGGCGCAA 600
DB 541 TTCTTTGCTCTGCTGCTCATCATCATCTCTGTGTCTACTCTGCGCATCTCAAGGCGCAA 600
QY 601 GCGGCAACCGCGAGAGGTCCAGGCGCGCAAGGCGCGCGCTGCGCGAGGTGATCAAGCAG 660
DB 601 GCGGCAACCGCGAGAGGTCCAGGCGCGCAAGGCGCGCGCTGCGCGAGGTGATCAAGCAG 660
QY 661 CCGCGACCCGACCATGTGTGCGCGCTTTGCGCTCAAGCAGGCGCGCGCTGCGCGAG 720
DB 661 CCGCGACCCGACCATGTGTGCGCGCTTTGCGCTCAAGCAGGCGCGCGCTGCGCGAG 720
QY 721 GCTTTGCGCAAGAGGTGCAAGGAGCATCTCAAGGCGCGCGCTGCGCGAGGAGGAGGAG 780
DB 721 GCTTTGCGCAAGAGGTGCAAGGAGCATCTCAAGGCGCGCGCTGCGCGAGGAGGAGGAG 780
QY 781 ACCCTGGAAGTACTGAGAGCCCGCGCTTGCACCCAGTTGGCTGGCTTCCCACTCA 840
DB 781 ACCCTGGAAGTACTGAGAGCCCGCGCTTGCACCCAGTTGGCTGGCTTCCCACTCA 840
QY 841 GCGCGAGGCGCGAGAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 GCGCGAGGCGCGAGAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 TCACTTGAAGCCCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TCACTTGAAGCCCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GCGCGAGGTGCTCTGCGCGAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
DB 1021 GCGCGAGGTGCTCTGCGCGAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
QY 1081 GCGCGAGGTGCTCTGCGCGAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1081 GCGCGAGGTGCTCTGCGCGAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 1141 GTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
DB 1141 GTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
QY 1201 TGCAAGGTGCGCGAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
DB 1201 TGCAAGGTGCGCGAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1261 CTGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
DB 1261 CTGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 1321 CTGTGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
DB 1321 CTGTGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
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RESULT 2

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US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulou, Markku
; APPLICANT: Pesonen, Ulla-Mari
; APPLICANT: Scheinin, Mika
; APPLICANT: Tuomola, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Myllynen, Kristina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kaanen, Uusi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/422,985
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
; OTHER INFORMATION: protein
; US-09-825-923-3

Query Match 96.2%; Score 1302; DB 9; Length 1353;
Best Local Similarity 99.9%; Freq. No. 0; Mismatches 1; Indels 0; Gaps 0;
Matches 1352; Conservative

QY 1 ATGAGCAACACAGACCCCTACTCCGTGAGGCGCAAGGCGCGCATAGCGCGCGCATAC 60
DB 1 ATGAGCAACACAGACCCCTACTCCGTGAGGCGCAAGGCGCGCATAGCGCGCGCATAC 60
QY 61 TTCTCATTTCTTTTACCACTTTTGGGCAAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 TTCTCATTTCTTTTACCACTTTTGGGCAAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 GGTGCGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 GGTGCGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 GTGCGCAAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 181 GTGCGCAAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 241 GGTGCGCAAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 GGTGCGCAAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 GTGCACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 301 GTGCACTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 AACTCAAGGCGACCCCGCGCGCATCAAGTGCATCATCTCTCATCTGTGTGCTCATGCCC 420
DB 361 AACTCAAGGCGACCCCGCGCGCATCAAGTGCATCATCTCTCATCTGTGTGCTCATGCCC 420
QY 421 GCGGTATCTGCTGCGCGCCCTCATCTCAAGGCGGACCAAGGCGCCGCGCGCGG 480
DB 421 GCGGTATCTGCTGCGCGCCCTCATCTCAAGGCGGACCAAGGCGCCGCGCGCGG 480
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QY 481 CCCCCAGTGAAGCTCAACGAGAGGCTGTACATCTGTGCTCCAGCATTCGATCT 540
DB 481 CCCCCAGTGAAGCTCAACGAGAGGCTGTACATCTGTGCTCCAGCATTCGATCT 540
QY 541 TTCTTGTCTCTTGTCTCATATGATCTTTGTCTACCTGCGCATCTGATTCGCAAA 600
DB 541 TTCTTGTCTCTTGTCTCATATGATCTTTGTCTACCTGCGCATCTGATTCGCAAA 600
QY 601 CGCAGCAACCGAGAGGTCCGAGGGCCGAGGGGGGGCTGGGCGAGGGTGAATCCAGCAG 660
DB 601 CGCAGCAACCGAGAGGTCCGAGGGCCGAGGGGGGGCTGGGCGAGGGTGAATCCAGCAG 660
QY 661 CCCCCAGTGAAGCTCAACGAGAGGCTGTGCTCAAGCCAACTGCGAGCCCTGTCTGTG 720
DB 661 CCCCCAGTGAAGCTCAACGAGAGGCTGTGCTCAAGCCAACTGCGAGCCCTGTCTGTG 720
QY 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCCACTGGGGAGAGAGAGAGGGGAG 780
DB 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCCACTGGGGAGAGAGAGAGGGGAG 780
QY 781 ACCCTGAAGATATCTGGGACCCGGGCTTGGCCAACTGGGGCTGCTTCCCACTCA 840
DB 781 ACCCTGAAGATATCTGGGACCCGGGCTTGGCCAACTGGGGCTGCTTCCCACTCA 840
QY 841 GGCAGAGGCGAGAGAGGAGTGTGTTGTGGGGCATCTCGAGAGATGAAGCTGAAGAGAG 900
DB 841 GGCAGAGGCGAGAGAGGAGTGTGTTGTGGGGCATCTCGAGAGATGAAGCTGAAGAGAG 900
QY 901 GAAAGAGAGAGAGAGAGAGAGAGTGTGAACCCGAGGCACTGCGAGTCTCCGAGCC 960
DB 901 GAAAGAGAGAGAGAGAGAGAGAGTGTGAACCCGAGGCACTGCGAGTCTCCGAGCC 960
QY 961 TGAAGCTTGAAGCCCCCGCTGCGAGAGCCAGAGGCTCCCGGGTGTGGCCACCTACGT 1020
DB 961 TGAAGCTTGAAGCCCCCGCTGCGAGAGCCAGAGGCTCCCGGGTGTGGCCACCTACGT 1020
QY 1021 GGCAGAGTCTCTGTGGGCGAGGGGCGTGTGCTATGAGTGGGAGTGGGGTGGAGAG 1080
DB 1021 GGCAGAGTCTCTGTGGGCGAGGGGCGTGTGCTATGAGTGGGAGTGGGGTGGAGAG 1080
QY 1081 GCGCAGCTGACCCGAGAGAGAGGCTTCACTTCTGTGCTGCTGTGTGCTATTTT 1140
DB 1081 GCGCAGCTGACCCGAGAGAGAGGCTTCACTTCTGTGCTGCTGTGTGCTATTTT 1140
QY 1141 GTGCTGTGCTGCTTCTTCTTCTTCACTCAAGCTGTGGGGCGCATCTGCCGAGAC 1200
DB 1141 GTGCTGTGCTGCTTCTTCTTCTTCACTCAAGCTGTGGGGCGCATCTGCCGAGAC 1200
QY 1201 TGCAGAGTCCCGCATGAGGCTCTTCCAGTCTTCTGTGATGAGGCTACTGCAACAGCTCA 1260
DB 1201 TGCAGAGTCCCGCATGAGGCTCTTCCAGTCTTCTGTGATGAGGCTACTGCAACAGCTCA 1260
QY 1261 CTGAACCTCTTATCTCAACCATCTTCAACAGAGATTTCCGCCGTGCTTCCGAGAGATC 1320
DB 1261 CTGAACCTCTTATCTCAACCATCTTCAACAGAGATTTCCGCCGTGCTTCCGAGAGATC 1320
QY 1321 CTGTGCGGCGCGTGAACCCAGAGAGGCTGTGA 1353
DB 1321 CTGTGCGGCGCGTGAACCCAGAGAGGCTGTGA 1353
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RESULT 3
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salomon, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
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; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match          96.2%; Score 1302; DB 15; Length 1353;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 1 ATGAAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 61 TTCTTATCTCTTATCAATCTTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 61 TTCTTATCTCTTATCAATCTTTCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 CGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 CGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 GTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 CGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 CGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 GTGCACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 GTGCACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 AACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 AACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GCGGCTATCTCGCTGCGGCTCTCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GCGGCTATCTCGCTGCGGCTCTCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 CCCCCAGTGAAGCTCAACGAGAGGCTGTGATCATCTGGGCTCCAGCATTCGATCT 540
DB 481 CCCCCAGTGAAGCTCAACGAGAGGCTGTGATCATCTGGGCTCCAGCATTCGATCT 540
QY 541 TTCTTGTCTCTTGTCTCATATGATCTTTGTCTACCTGCGCATCTGATTCGCAAA 600
DB 541 TTCTTGTCTCTTGTCTCATATGATCTTTGTCTACCTGCGCATCTGATTCGCAAA 600
QY 601 CGCAGCAACCGAGAGGTCCGAGGGCCGAGGGGGGGCTGGGCGAGGGTGAATCCAGCAG 660
DB 601 CGCAGCAACCGAGAGGTCCGAGGGCCGAGGGGGGGCTGGGCGAGGGTGAATCCAGCAG 660
QY 661 CCCCCAGTGAAGCTCAACGAGAGGCTGTGCTCAAGCCAACTGCGAGCCCTGTCTGTG 720
DB 661 CCCCCAGTGAAGCTCAACGAGAGGCTGTGCTCAAGCCAACTGCGAGCCCTGTCTGTG 720
QY 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCCACTGGGGAGAGAGAGAGGGGAG 780
DB 721 GCTTCTGCGAGAGGTCAACGAGCACTCGAAGTCCACTGGGGAGAGAGAGAGGGGAG 780
QY 781 ACCCTGAAGATATCTGGGACCCGGGCTTGGCCAACTGGGGCTGCTTCCCACTCA 840
DB 781 ACCCTGAAGATATCTGGGACCCGGGCTTGGCCAACTGGGGCTGCTTCCCACTCA 840
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Db      1613  TGCAGAGTGCCCAATAGGCTCTTCACAGTTCTTCTTCGTGATCGGCTACTCGACAAGCTCA 1672
Oy      1261  CTGAACCTCTGTATCTACACCATCTTCAACGAGACTTCGCGCGCTTCCGGAGATC 1320
Db      1673  CTGAACCCCTGTATCTACACCATCTTCAACGAGACTTCGCGCGCTTCCGGAGATC 1732
Oy      1321  CTGTGCGCGCCGTGGAGCCAGACGGCCCTGTGTA 1353
Db      1733  CTGTGCGCGCCGTGGAGCCAGACGGCCCTGTGTA 1765

RESULT 5
US-10-225-567A-41
: Sequence 41, Application US/10225567A
: Publication No. US20030113798A1
: GENERAL INFORMATION:
: APPLICANT: Lifespan BioSciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burmet, Glenn C.
: TITLE OF INVENTION: Antigenic L.
: FILE REFERENCE: 1920-4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: PRIOR FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/257,144
: NUMBER OF SEQ ID NOS: 2392
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 41
: LENGTH: 3274
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-225-567A-41

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| QY | 541 | TTCTTTGTCCTTCCTCCATCATCATATGATCTTGTCTACCTGGCGCATCTACCTGATGCGCAAA | 600 |
| Db | 541 | TTCTTTGTCTTCTTCTCTCATCATATATCTTGTCTACTCTGGCATCTACCTGATGCGCAAA | 600 |
| QY | 601 | CGCAGCAACCGCAGAGGTCCCGAGGCCAAGGCGGGGCGCTGCGGCAGGGGTGAGTCCAGCAG | 660 |
| Db | 601 | CGCAGCAACCGCAGAGGTCCCGAGGGCCAGAGGGGGGGCGTGGGCAGGGGTGAGTCCAGCAG | 660 |
| QY | 661 | CCCCGACCCCAACCATTGGTGGGGGCTTTTGGCTCTAGCCCAAATTGCCAGGCCCTGGCTCTGTG | 720 |
| Db | 661 | CCCCGACCCCAACCATTGGTGGGGGCTTTTGGCTCTAGCCCAAATCTGAGCCCTGGGCTCTGTG | 720 |
| QY | 721 | GCTTCTGCGAGAGAGGTCTAACCGGACCTCGAAGTCCACTGGGGGAGAGAGAGAGAGGGGGAG | 780 |
| Db | 721 | GCTTCTGCGAGAGAGGTCTAACCGGACCTCGAAGTCCACTGGGGGAGAGAGAGAGAGGGGGAG | 780 |
| QY | 781 | ACCCCTGAAGATACTGGGACCCCGGGCCTTGTGCACCCAGTGGGCTGTGCCCTTCCCACTCA | 840 |
| Db | 781 | ACCCCTGAAGATACTGGGACCCCGGGCCTTGTGCACCCAGTGGGCTGTGCCCTTCCCACTCA | 840 |
| QY | 841 | GGCCAGGGCCCAAGAGAGGGGTGTTTGTGGGGCACTCTCAGAGATGAAAGCTGMAAGAGAG | 900 |
| Db | 841 | GGCCAGGGCCCAAGAGAGGGGTGTTTGTGGGGCACTCTCAGAGATGAAAGCTGMAAGAGAG | 900 |
| QY | 901 | GAAAGAGAGAGAGAGAGAGAGATGTGMAACCCAGGCGAGTGCACGTCTCCGAGCC | 960 |
| Db | 901 | GAAAGAGAGAGAGAGAGAGAGATGTGMAACCCAGGCGAGTGCACGTCTCCGAGCC | 960 |
| QY | 961 | TCAGCTTGCAGGCCCCCGCTGCAGCAGCACAGGGCTCCCGGGTGTCTGGCCACTCTACGT | 1020 |
| Db | 961 | TCAGCTTGCAGGCCCCCGCTGCAGCAGCACAGGGCTCCCGGGTGTCTGGCCACTCTACGT | 1020 |
| QY | 1021 | GGCCAGGGGTCTCCGGGCGAGGGGGGTGAGGGTCTATAGGTGGGCGAGTGTGGCGCTCGAAGG | 1080 |
| Db | 1021 | GGCCAGGGGTCTCTGGGGCGAGGGGGGTGAGGGTCTATAGGTGGGCGAGTGTGGCGCTCGAAGG | 1080 |
| QY | 1081 | GCGCAGCTGACCCCGGAGAAAGCGCTTACACTTCGTGCTGAGCTGTGATTCATTGGCGTTTTT | 1140 |
| Db | 1081 | GCGCAGCTGACCCCGGAGAAAGCGCTTACACTTCGTGCTGAGCTGTGATTCATTGGCGTTTTT | 1140 |
| QY | 1141 | GTGCTCTGCTGTGTTCCCTCTTCTTTCAAGCTACAGCTCGTGGGCGCATCTGCGGCAACAC | 1200 |
| Db | 1141 | GTGCTCTGCTGTGTTCCCTCTTCTTTCAAGCTACAGCTCGTGGGCGCATCTGCGGCAACAC | 1200 |
| QY | 1201 | TGCAAGGAGGCCCATAGGAGCTCTTCCAGTCTCTTCTGTGATGCGCTACTGCAACAGCTCA | 1260 |
| Db | 1201 | TGCAAGGAGGCCCATAGGAGCTCTTCCAGTCTCTTCTGTGATGCGCTACTGCAACAGCTCA | 1260 |
| QY | 1261 | CTGAACCCCTGTATCTACACCATTTCAACCAAGGACTTCCGCGGTGCTTCCGAGGATC | 1320 |
| Db | 1261 | CTGAACCCCTGTATCTACACCATTTCAACCAAGGACTTCCGCGGTGCTTCCGAGGATC | 1320 |
| QY | 1321 | CTGTGCGCGCCGTGAGACCCAGACGGCCTGTGGTGA | 1353 |
| Db | 1321 | CTGTGCGCGCCGTGAGACCCAGACGGCCTGTGGTGA | 1353 |

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RESULT 6
US-09-825-923-1
; Sequence 1, Application US/098259231
; Patent No. US2001001638A1
; GENERAL INFORMATION
; APPLICANT: Snäppl, Amir
; APPLICANT: Heimonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Metti
; APPLICANT: Koulun, Markku
; APPLICANT: Pesonen, Ulla-Mari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A

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Db      |||||||
361  AACTCAGACGACCCCGCGCCGATCAAGTGCATCTCATCTGTGTGCTCATTCGCC 420
Qy      |||||||
421  GCGGTATCTGCTGCGCGCCCTCATCTCAAGGGGACACAGGGCCCCAGCGCGGG 480
Db      |||||||
421  GCGGTATCTGCTGCGCGCCCTCATCTCAAGGGGACACAGGGCCCCAGCGCGGG 480
Qy      |||||||
481  GCGCCCAAGTGAAGTCAACAGAGAGGCTGTATCATCTGAGCTTCAGCATCGATCT 540
Db      |||||||
481  GCGCCCAAGTGAAGTCAACAGAGAGGCTGTATCATCTGAGCTTCAGCATCGATCT 540
Qy      |||||||
541  TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTGATCGCAAA 600
Db      |||||||
541  TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTGATCGCAAA 600
Qy      |||||||
601  GCGCAGCAACCGAGAGGTCTCCAGGGGCGAGGGGGGGCTGGGAGGATGTCAGAG 660
Db      |||||||
601  GCGCAGCAACCGAGAGGTCTCCAGGGGCGAGGGGGGGCTGGGAGGATGTCAGAG 660
Qy      |||||||
661  CCCCGACCCGACCATGTGTGGGCTTTGGCTCAGCCAACTGCGAGCCCTGGCTGTG 720
Db      |||||||
661  CCCCGACCCGACCATGTGTGGGCTTTGGCTCAGCCAACTGCGAGCCCTGGCTGTG 720
Qy      |||||||
721  GCTTGTCCAGAGAGTCAACGAGCACTCGAAGTCCACTGCGAGAGAGAGAGAGAG 780
Db      |||||||
721  GCTTGTCCAGAGAGTCAACGAGCACTCGAAGTCCACTGCGAGAGAGAGAGAGAG 780
Qy      |||||||
781  ACCCTGAAAGATCTAGGACCCGGGCTTGGCCACCAAGTTGGCTGCTTCCCACTCA 840
Db      |||||||
781  ACCCTGAAAGATCTAGGACCCGGGCTTGGCCACCAAGTTGGCTGCTTCCCACTCA 840
Qy      |||||||
841  GCGCAGGGGCGAGAGAGGCTTTGTGGGGCATCTCCAGAGATGAAGTGAAGAGAG 900
Db      |||||||
841  GCGCAGGGGCGAGAGAGGCTTTGTGGGGCATCTCCAGAGATGAAGTGAAGAGAG 900
Qy      |||||||
901  GAAAGAGAGAGAGAGAG 918
Db      |||||||
901  GAAAGAGAGAGAGAGAG 918

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RESULT 8

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; Sequence 2, Application US/1001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-001-073-2

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Query Match 66.7%; Score 902; DB 15; Length 1344;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGACACACAGAGACCCCTACTCTCGTGACGACCAAGCGGCATAGCGGCGCATCAC 60
Db      1 ATGACACACAGAGACCCCTACTCTCGTGACGACCAAGCGGCATAGCGGCGCATCAC 60
Qy      61 TTCCATATCTCTTAAACATCTTGGGACAGCTCTGTGATCTCTGCTGTGTGACCAAC 120
Db      61 TTCCATATCTCTTAAACATCTTGGGACAGCTCTGTGATCTCTGCTGTGTGACCAAC 120
Qy      121 CGCTGCTGCGGCGCCCTCAGAACCTGTCTGTGTGCTGCTGCGCGCGCAGCATCTCG 180

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Db      |||||||
121  CGCTGCTGCGGCGCCCTCAGAACCTGTCTGTGTGCTGCTGCGCGCGCGCAGCATCTCG 180
Qy      |||||||
181  GTGGCAGAGCTCATATCCCTTCTGCTGAGCAAGAGACTGTGGGCTACTGTACTTC 240
Db      |||||||
181  GTGGCAGAGCTCATATCCCTTCTGCTGAGCAAGAGACTGTGGGCTACTGTACTTC 240
Qy      |||||||
241  CGGCGCAGTGTGGAGAGGTGTACTGTGGGCTGACAGGTCTTCTGACCTGTTCATC 300
Db      |||||||
241  CGGCGCAGTGTGGAGAGGTGTACTGTGGGCTGACAGGTCTTCTGACCTGTTCATC 300
Qy      |||||||
301  GTGACCTGTGTGCGCATCAGGCTGAGACGCTGCTGAGAGGCTGAGAGTAC 360
Db      |||||||
301  GTGACCTGTGTGCGCATCAGGCTGAGACGCTGCTGAGAGGCTGAGAGTAC 360
Qy      |||||||
361  AACTCAGACGACCCCGCGCCGATCAAGTGCATCTCATCTGTGTGCTCATTCGCC 420
Db      |||||||
361  AACTCAGACGACCCCGCGCCGATCAAGTGCATCTCATCTGTGTGCTCATTCGCC 420
Qy      |||||||
421  GCGGTATCTGCTGCGCGCCCTCATCTCAAGGGGACACAGGGCCCCAGCGCGGG 480
Db      |||||||
421  GCGGTATCTGCTGCGCGCCCTCATCTCAAGGGGACACAGGGCCCCAGCGCGGG 480
Qy      |||||||
481  GCGCCCAAGTGAAGTCAACAGAGAGGCTGTATCATCTGAGCTTCAGCATCGATCT 540
Db      |||||||
481  GCGCCCAAGTGAAGTCAACAGAGAGGCTGTATCATCTGAGCTTCAGCATCGATCT 540
Qy      |||||||
541  TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTGATCGCAAA 600
Db      |||||||
541  TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTGATCGCAAA 600
Qy      |||||||
601  GCGCAGCAACCGAGAGGTCTCCAGGGGCGAGGGGGGGCTGGGAGGATGTCAGAG 660
Db      |||||||
601  GCGCAGCAACCGAGAGGTCTCCAGGGGCGAGGGGGGGCTGGGAGGATGTCAGAG 660
Qy      |||||||
661  CCCCGACCCGACCATGTGTGGGCTTTGGCTCAGCCAACTGCGAGCCCTGGCTGTG 720
Db      |||||||
661  CCCCGACCCGACCATGTGTGGGCTTTGGCTCAGCCAACTGCGAGCCCTGGCTGTG 720
Qy      |||||||
721  GCTTGTCCAGAGAGTCAACGAGCACTCGAAGTCCACTGCGAGAGAGAGAGAGAG 780
Db      |||||||
721  GCTTGTCCAGAGAGTCAACGAGCACTCGAAGTCCACTGCGAGAGAGAGAGAGAG 780
Qy      |||||||
781  ACCCTGAAAGATCTAGGACCCGGGCTTGGCCACCAAGTTGGCTGCTTCCCACTCA 840
Db      |||||||
781  ACCCTGAAAGATCTAGGACCCGGGCTTGGCCACCAAGTTGGCTGCTTCCCACTCA 840
Qy      |||||||
841  GCGCAGGGGCGAGAGAGGCTTTGTGGGGCATCTCCAGAGATGAAGTGAAGAGAG 900
Db      |||||||
841  GCGCAGGGGCGAGAGAGGCTTTGTGGGGCATCTCCAGAGATGAAGTGAAGAGAG 900
Qy      |||||||
901  GA 902
Db      |||||||
901  GA 902

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RESULT 9

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; US-09-908-975-4848
; Sequence 4848, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607

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PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4848
LENGTH: 65
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-908-975-4848

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-21; Length 65;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 GCAGGTCATGCCAGAGCCCGAGCCGACATGTCGGGCTTTGGCTTACGCAACT 701
DB 1 GCAGGTCATGCCAGAGCCCGAGCCGACATGTCGGGCTTTGGCTTACGCAACT 60
QY 702 GCCAG 706
DB 61 GCCAG 65

RESULT 10
US-09-908-975-19227
Sequence 19227, Application US/09908975
Publication No. US20030165843A1

GENERAL INFORMATION:
APPLICANT: SHOSHAN, Av1
APPLICANT: MASSEMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FAJGIER, Simcha
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICER
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19227
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-19227

Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-19; Length 60;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 698 AACTGCCAGCCCTGGCTTCTGTCGAGAGAGTCAAGGACATCGACATCGCAAGTCCA 757
DB 1 AACTGCCAGCCCTGGCTTCTGTCGAGAGAGTCAAGGACATCGACATCGCAAGTCCA 60

RESULT 11
US-10-001-073-24
Sequence 24, Application US/10001073
Publication No. US20030113725A1

GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 1350

TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-24

Query Match
Best Local Similarity 100.0%; Pred. No. 7.8e-12; Length 1350;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATCGTCGACCTGTGGCCGATCAGCTGACCGCTACTGG 336
DB 355 TCGTCATCGTCGACCTGTGGCCGATCAGCTGACCGCTACTGG 399

RESULT 12
US-10-001-073-25
Sequence 25, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION NUMBER: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 1350
TYPE: DNA
ORGANISM: Homo sapiens
US-10-001-073-25

Query Match
Best Local Similarity 100.0%; Pred. No. 7.8e-12; Length 1350;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATCGTCGACCTGTGGCCGATCAGCTGACCGCTACTGG 336
DB 355 TCGTCATCGTCGACCTGTGGCCGATCAGCTGACCGCTACTGG 399

RESULT 13
US-10-305-720-1180
Sequence 1180, Application US/10305720
Publication No. US20040010136A1

GENERAL INFORMATION:
APPLICANT: An-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1180
LENGTH: 3604
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g178195
US-10-305-720-1180

Query Match
Best Local Similarity 100.0%; Pred. No. 6.9e-12; Length 3604;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATCGTCGACCTGTGGCCGATCAGCTGACCGCTACTGG 336
DB 2432 TCGTCATCGTCGACCTGTGGCCGATCAGCTGACCGCTACTGG 2476

RESULT 14
 US-10-225-567A-39
 ; Sequence 39; Application US/10225567A
 ; Publication No. US2003013798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lifespan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burner, Glenn C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 39
 ; LENGTH: 3653
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-225-567A-39

Query Match 3.3%; Score 45; DB 15; Length 3653;
 Best Local Similarity 100.0%; Pred. No. 6.9e-12;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCCTCATGCTGACCTGTGCGCCATCAGCTGACCGCTACTGG 336
 DB 1234 TCCTCATGCTGACCTGTGCGCCATCAGCTGACCGCTACTGG 1278

RESULT 15
 US-09-918-995-29557
 ; Sequence 29557; Application US/09918995
 ; Publication No. US20030073623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/918,995
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: US/09/235,076
 ; PRIOR FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 29557
 ; LENGTH: 463
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(463)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-918-995-29557

Query Match 2.9%; Score 39; DB 11; Length 463;
 Best Local Similarity 100.0%; Pred. No. 7.9e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1141 GTGCTGTGCTGCTTCCCTCTCTCTCAGCTACAGCTG 1179
 DB 51 GTGCTGTGCTGCTTCCCTCTCTCTCAGCTACAGCTG 89

Search completed: February 8, 2004, 06:56:26
 Job time : 521.217 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:51:07 / Search time 397.321 Seconds
(without alignments)
9192.405 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353

Sequence: 1 atgacaccagcagacccta.....ggaccacagacgctcgtcga 1353

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size: 30

Total number of hits satisfying chosen parameters: 79

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1353 | 100.0 | 1353 | 23 | AA199905 |
| 2 | 1302 | 96.2 | 1353 | 24 | AAD04762 |
| 3 | 1302 | 96.2 | 1353 | 24 | AAD04389 |
| 4 | 1251 | 92.5 | 2072 | 25 | AC156583 |
| 5 | 1251 | 92.5 | 3274 | 25 | AB242624 |
| 6 | 918 | 67.8 | 1344 | 22 | AAD04761 |
| 7 | 918 | 67.8 | 1344 | 24 | AAD44388 |
| 8 | 902 | 66.7 | 1344 | 23 | AA199906 |

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| 9 | 820 | 60.6 | 2064 | 12 | AAQ14151 |
| 10 | 820 | 60.6 | 2064 | 18 | AAT59499 |
| 11 | 65 | 4.8 | 65 | 24 | AEN32100 |
| 12 | 60 | 4.4 | 60 | 24 | ABN46479 |
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| 14 | 45 | 3.3 | 1350 | 23 | AA199918 |
| 15 | 45 | 3.3 | 3604 | 25 | ACA56582 |
| 16 | 45 | 3.3 | 3653 | 25 | AB242623 |
| 17 | 39 | 2.9 | 1382 | 15 | AAQ64890 |
| 18 | 39 | 2.9 | 1382 | 24 | AB235643 |
| 19 | 39 | 2.9 | 1382 | 25 | ACA56588 |
| 20 | 39 | 2.9 | 1758 | 24 | AB235339 |
| 21 | 36 | 2.7 | 215980 | 24 | AA138337 |
| 22 | 34 | 2.5 | 1171 | 23 | AA199933 |
| 23 | 34 | 2.5 | 1383 | 23 | AA199931 |
| 24 | 34 | 2.5 | 2826 | 25 | AB242625 |
| 25 | 33 | 2.4 | 1260 | 23 | AA569359 |
| 26 | 33 | 2.4 | 1260 | 23 | AA573144 |
| 27 | 33 | 2.4 | 1260 | 23 | AA575193 |
| 28 | 33 | 2.4 | 1563 | 24 | ABL53204 |
| 29 | 33 | 2.4 | 6904 | 24 | ABL32075 |
| 30 | 33 | 2.4 | 6904 | 24 | AA283865 |
| 31 | 32 | 2.4 | 224 | 23 | AA575432 |
| 32 | 32 | 2.4 | 1362 | 21 | AA49080 |
| 33 | 32 | 2.4 | 1756 | 21 | AA49091 |
| 34 | 32 | 2.4 | 1956 | 21 | AA38547 |
| 35 | 32 | 2.4 | 4519 | 21 | AA375260 |
| 36 | 32 | 2.4 | 5387 | 24 | AA239115 |
| 37 | 32 | 2.4 | 9803 | 22 | AAK79475 |
| 38 | 32 | 2.4 | 53226 | 25 | ABQ76896 |
| 39 | 30 | 2.2 | 171 | 22 | ABA74644 |
| 40 | 30 | 2.2 | 171 | 22 | AAK23115 |
| 41 | 30 | 2.2 | 171 | 22 | AAK49290 |
| 42 | 30 | 2.2 | 171 | 22 | AA155134 |
| 43 | 30 | 2.2 | 193 | 22 | ABA71654 |
| 44 | 30 | 2.2 | 193 | 22 | ABA37774 |
| 45 | 30 | 2.2 | 193 | 22 | AAK19996 |

ALIGNMENTS

RESULT 1
ID AA199905 standard; DNA; 1353 BP.
AA199905;
18-FEB-2002 (first entry)
Human alpha-2BAR third intracellular loop encoding DNA.
Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
polymorphic site; allelic variant; cardiovascular disease;
central nervous system disease; adenylyl cyclase; MAP kinase activity;
phosphorylation; inositol phosphate; alpha-2BAR;
Genbank Accession AF009500; chromosome 2; de.
Homo sapiens.
Key CDS
Location/Qualifiers
1.1353
/tag="a"
/product="alpha-2BAR"
/note="sequence includes a 9 nucleotide polymorphic site at nucleotides 901-909 absent in the alpha-2BAR variant (AA199906)"
MO200179561-A2.
25-OCT-2001.
17-APR-2001; 2001MO-US12575.

XX 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX LIGgett SB, Small KM;
PI MPI; 2001-611728/70.
DR P-PSDB; AAM52117.
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
PS Claim 4; Page 144; 163p; English.

XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C, or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (999GCG99GCG) or (B) (999GCGGCTGAG) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene, and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, the response
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phentolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlating the site to a
CC cycloase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BR (GenBank Accession AF09500), the sequence includes
CC a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the
CC alpha-2BAR variant (AAI99906).
XX
XX

SQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;

Query Match 100.0%; Score 1353; DB 23; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCACCAAGGACCCCTACTCCGAGAGGACAGACGCGCCATAGCGGGGCAATACC 60
DB 1 ATGAGCACCAAGGACCCCTACTCCGAGAGGACAGACGCGCCATAGCGGGGCAATACC 60
QY 61 TTCTCATTTCTTTTACCAATCTTGGCAACGCTTGATCATCTGCTGTGTGACAGC 120
DB 61 TTCTCATTTCTTTTACCAATCTTGGCAACGCTTGATCATCTGCTGTGTGACAGC 120
QY 121 CGCTGCTGCGCGCCCTCTAGAAACCTGTTCTGTGTGCTGCGCGCGCGCAATCTCTG 180
DB 121 CGCTGCTGCGCGCCCTCTAGAAACCTGTTCTGTGTGCTGCGCGCGCGCAATCTCTG 180
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DB 241 CGGCGCAGGTGGTGGAGGTGTAACCTGCGCTGACAGTGTCTTTCTGCAACCTGTCATC 300
QY 301 GTGACACTGTGTGGCATAGCCTGAGACCGCTTACTGGGCGGTGAGCGCGCTGAGTAC 360

DB 301 GTGACACTGTGTGGCATAGCCTGAGACCGCTTACTGGGCGGTGAGCGCGCTGAGTAC 360
QY 361 AACTCAAGCGGACCCCGCGCGCATCAAGTGCATCATCTCTCACTGTGTGCTCATCGCC 420
DB 361 AACTCAAGCGGACCCCGCGCGCATCAAGTGCATCATCTCTCACTGTGTGCTCATCGCC 420
QY 421 GCGCTCATCTGCTGCGCGCCCTCTCATCTCAAGGGGCAACAGGGCCCGCGCGCGG 480
DB 421 GCGCTCATCTGCTGCGCGCCCTCTCATCTCAAGGGGCAACAGGGCCCGCGCGCGG 480
QY 481 CGCGCCAGTGCAGCTCAACAGAGAGGCTGTACATCTGCTGCTCCAGCATCGATCT 540
DB 481 CGCGCCAGTGCAGCTCAACAGAGAGGCTGTACATCTGCTGCTCCAGCATCGATCT 540
QY 541 TTCTTTGCTCTGCTGCTCATATGATCTGTCTTCACTGCGCATTAACCTGATGCCAA 600
DB 541 TTCTTTGCTCTGCTGCTCATATGATCTGTCTTCACTGCGCATTAACCTGATGCCAA 600
QY 601 CGCAGCAACCGAGAGGTCCAGGGGCAAGGGGGGCTGGGCAAGGTGATCCAGCAG 660
DB 601 CGCAGCAACCGAGAGGTCCAGGGGCAAGGGGGGCTGGGCAAGGTGATCCAGCAG 660
QY 661 CCCGACCGGACCATGTGAGGCTTTTGGCTCAGCCAACTGCGAGCTGAGCTCTGTG 720
DB 661 CCCGACCGGACCATGTGAGGCTTTTGGCTCAGCCAACTGCGAGCTGAGCTCTGTG 720
QY 721 GCTTCTGCAAGAGGTCAAGGACCTGAAATCTGAGGAGAGAGAGAGAGAGAGAG 780
DB 721 GCTTCTGCAAGAGGTCAAGGACCTGAAATCTGAGGAGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAAGATCTAGGAGCCCGGCTTGGCAACCATGATGGGCTGCTCCCAATCA 840
DB 781 ACCCTGAAGATCTAGGAGCCCGGCTTGGCAACCATGATGGGCTGCTCCCAATCA 840
QY 841 GGCAGGGGCAAGAGAGAGGTGTTGTGGGGCATCTCCAGAGATGAAAGAGAGAG 900
DB 841 GGCAGGGGCAAGAGAGAGGTGTTGTGGGGCATCTCCAGAGATGAAAGAGAGAG 900
QY 901 GAAAG 960
DB 901 GAAAG 960
QY 961 TCAGCTTCAAGCCCGCTGCTCAGAGAGCAGAGAGGCTCCGGGTGTGGCCACCTTACGT 1020
DB 961 TCAGCTTCAAGCCCGCTGCTCAGAGAGCAGAGAGGCTCCGGGTGTGGCCACCTTACGT 1020
QY 1021 GACCAAGTGTCTCTGGGCAAGGAGGCTGTGGGTCTTATAGGTGGCAAGTGTGAGG 1080
DB 1021 GACCAAGTGTCTCTGGGCAAGGAGGCTGTGGGTCTTATAGGTGGCAAGTGTGAGG 1080
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DB 1081 GCGAGAGTGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 GTGCTGTGTGTGTTCCCTTTCTTCTGAGCTCAAGCTTGGGCGCATCTGCGCAAGC 1200
DB 1141 GTGCTGTGTGTGTTCCCTTTCTTCTGAGCTCAAGCTTGGGCGCATCTGCGCAAGC 1200
QY 1201 TGCAGAGTGCAG 1260
DB 1201 TGCAGAGTGCAG 1260
QY 1261 CTGAACCTGTATCTAACAACATCTTCAACAGAGATCTCCGCGCTTCCGAGATC 1320
DB 1261 CTGAACCTGTATCTAACAACATCTTCAACAGAGATCTCCGCGCTTCCGAGATC 1320
QY 1321 CTGTGCGCGCGGTGAGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383
DB 1321 CTGTGCGCGCGGTGAGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383

RESULT 2

AAD04762
 ID AAD04762 standard; DNA; 1353 BP.
 AC AAD04762;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
 XX
 KM Human; carotid; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KM glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KM noradrenaline; epinephrine; therapy; vascular contraction;
 KM coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KM acute myocardial infarction; AMI; Prinzmetal's variant; de.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /*tag= a
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 FT protein"
 XX
 PN WO200129082-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000WO-FI00913.
 XX
 PR 22-OCT-1999; 99US-0422985.
 XX
 PA (JUVA-) JUVAANTIA PHARMA LTD OY.
 XX
 PI Snapiir A, Heinonen P, Alhopuro P, Karvonen M, Koulou M, Pesonen U;
 PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Myysoenen K;
 PI Salonen R, Kahanen J, Valkonen V;
 XX
 DR MPI: 2001-300318/31.
 DR P-PSDB; AAE00990.
 XX
 PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 PS Disclosure; Page 27-29; 37pp; English.
 XX
 CC The present sequence is a gene encoding human alpha2B-adrenoceptor
 CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
 CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
 CC acids (amino acids 294-311), located in the third intracellular loop of
 CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
 CC Alpha2-AR mediate many of the physiological effects of the
 CC catecholamines, norepinephrine and epinephrine. An antagonist of
 CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
 CC vascular contraction of coronary arteries and a disease involving
 CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
 CC clinically expressed as Prinzmetal's variant form or acute myocardial
 CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
 XX
 SO Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
 Query Match 96.2%; Score 1302; DB 22; Length 1353;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ATGAGACACGAGACCCCTACTCCGTCAGGCGGACGAGCCCTTACGGGCGGCATCACC 60
 DB 1 ATGAGACACGAGACCCCTACTCCGTCAGGCGGACGAGCCCTTACGGGCGGCATCACC 60
 QY 61 TTCCTCATCTCTTACCATCTTGGCAAGCTGTGATCCTGCTGCTGTGATGACGAGC 120
 DB 61 TTCCTCATCTCTTACCATCTTGGCAAGCTGTGATCCTGCTGCTGTGATGACGAGC 120

Db 61 TTCCTCATCTCTTACCATCTTGGCAAGCTGTGATCCTGCTGCTGTGATGACGAGC 120
 QY 121 CGCTGCTGCGGCGCCCTCAGAACTGTTCTGTGTGCTGCGCGCGCGCATCTCTG 180
 Db 121 CGCTGCTGCGGCGCCCTCAGAACTGTTCTGTGTGCTGCGCGCGCGCATCTCTG 180
 QY 181 GTGGCAGCCTCATCATCTCTTCTGTCGCGCAAGCTGTGCGGCTACTGTACTTC 240
 Db 181 GTGGCAGCCTCATCATCTCTTCTGTCGCGCAAGCTGTGCGGCTACTGTACTTC 240
 QY 241 CGGCGCAGTGTGTGCGAGGTGTACTGTGCGCTGAGCTGTCTTCTGCACTCTGTCATC 300
 Db 241 CGGCGCAGTGTGTGCGAGGTGTACTGTGCGCTGAGCTGTCTTCTGCACTCTGTCATC 300
 QY 301 GTGCACTGTGCGGCGCATCATGCGCTGAGCGGCTACTGTGCGCGCGGCTGAGTAC 360
 Db 301 GTGCACTGTGCGGCGCATCATGCGCTGAGCGGCTACTGTGCGCGCGGCTGAGTAC 360
 QY 361 AACTCCAGCGGACCCCGCGCGCATCATGAGTGCATCTCTCACTGTGTGCTCATCGCC 420
 Db 361 AACTCCAGCGGACCCCGCGCGCATCATGAGTGCATCTCTCACTGTGTGCTCATCGCC 420
 QY 421 GCGGTATCTCGCTGCGCGCGCTCATCTCAAGGCGGACGAGCGCGCGCGCGG 480
 Db 421 GCGGTATCTCGCTGCGCGCGCTCATCTCAAGGCGGACGAGCGCGCGCGCGG 480
 QY 481 CGCGCCAGTGTGAGGTCAACGAGGCGCTGTATCTGTGCGCTCCAGCATCGGATCT 540
 Db 481 CGCGCCAGTGTGAGGTCAACGAGGCGCTGTATCTGTGCGCTCCAGCATCGGATCT 540
 QY 541 TTCTTGTCTCTGCTCATCATGATCTTGTGTACTGTCGCGCATCTTACCTGACCA 600
 Db 541 TTCTTGTCTCTGCTCATCATGATCTTGTGTACTGTCGCGCATCTTACCTGACCA 600
 QY 601 CGGAGCAACCGGAGAGGTCTCCAGGCGCAAGGCGGCGCTGTGCGGAGGTATCAAGCAG 660
 Db 601 CGGAGCAACCGGAGAGGTCTCCAGGCGCAAGGCGGCGCTGTGCGGAGGTATCAAGCAG 660
 QY 661 CCCCGACCGGACCATGTGCGGCTTGTGCTGAGCGCAACCTGCGACCGCTGCGCTGTG 720
 Db 661 CCCCGACCGGACCATGTGCGGCTTGTGCTGAGCGCAACCTGCGACCGCTGCGCTGTG 720
 QY 721 GCTTTCGACAGAGGTCAACGAGCACTGGAAGTCACTGTGCGGAGAGAGAGAGAG 780
 Db 721 GCTTTCGACAGAGGTCAACGAGCACTGGAAGTCACTGTGCGGAGAGAGAGAGAGAG 780
 QY 781 ACCCTGGAAGATATCTGGAACCGGCGCTTGCACCCAGTGTGCGCTTCCCACTCA 840
 Db 781 ACCCTGGAAGATATCTGGAACCGGCGCTTGCACCCAGTGTGCGCTTCCCACTCA 840
 QY 841 GGCAGGCGCAAGAGAGGTGTTGTGCGGCTTCTCCAGAGATGAAGCTGAAGAGAG 900
 Db 841 GGCAGGCGCAAGAGAGGTGTTGTGCGGCTTCTCCAGAGATGAAGCTGAAGAGAG 900
 QY 901 GAAAGGAGAGAGAGAGAGAGAGTGAACCCAGGAGTGCAGTGTCTCCGCGC 960
 Db 901 GAAAGGAGAGAGAGAGAGAGTGAACCCAGGAGTGCAGTGTCTCCGCGC 960
 QY 961 TCAGCTTGAAGCGCCCGCTGAGCAGCAGAGGCTCCCGGCTGTGCGCACTTACGT 1020
 Db 961 TCAGCTTGAAGCGCCCGCTGAGCAGCAGAGGCTCCCGGCTGTGCGCACTTACGT 1020
 QY 1021 GGCAGGTGCTCTGTGCGGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
 Db 1021 GGCAGGTGCTCTGTGCGGCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
 QY 1081 GGCAGGTGACCCGAGAGAGAGGCTTACCTTGTGTGTGTGTGTGTGTGTGTGT 1140
 Db 1081 GGCAGGTGACCCGAGAGAGAGGCTTACCTTGTGTGTGTGTGTGTGTGTGTGT 1140
 QY 1141 GTGCTGT 1200
 Db 1141 GTGCTGT 1200

QY 1201 TGCAGATGCCCCATGAGCTCTTTCAGATTCTTCTTGATCGGCTACTGCAACAGCTCA 1260
Db 1201 TGAAGGTGCCCCATGAGCTCTTTCAGATTCTTCTTGATCGGCTACTGCAACAGCTCA 1260
QY 1261 CTGAACCCCTGTATCTTACACCATCTTCAACAGAGACTTCGCGCTGCTTCCGAGAGATC 1320
Db 1261 CTGAACCCCTGTATCTTACACCATCTTCAACAGAGACTTCGCGCTGCTTCCGAGAGATC 1320
QY 1321 CTGTGCGCCCGTGAAGCCGAGAGGCTGTGTA 1353
Db 1321 CTGTGCGCCCGTGAAGCCGAGAGGCTGTGTA 1353
RESULT 3
AAD4389
ID AAD4389 standard; DNA; 1353 BP.
AC AAD4389;
XX
XX 13-DEC-2002 (first entry)
DT 13-DEC-2002 (first entry)
XX
XX Human alpha-2B-adrenoceptor gene.
DE Human alpha-2B-adrenoceptor gene.
XX
XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KM hypertension; hypotensive; gene; ds.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a
FT /product= "Human alpha-2B-adrenoceptor protein"
XX
XX MO200266617-A1.
XX
XX 29-AUG-2002.
PD 13-FEB-2002; 2002MO-F100113.
XX
XX 20-FEB-2001; 2001FI-0000323.
PR (JURI-) JURILAB LTD OY.
XX
XX Salonen J;
PI MPI; 2002-667063/71.
XX
XX P-PSDB; AAE26534.
DR
XX
XX Detecting a risk of hypertension and targeting treatment in a subject
XX by determining the pattern of alleles encoding a variant
XX alpha-2-adrenoceptor -
XX
XX Disclosure; Page 27-29; 35pp; English.
XX
XX The invention relates to a method for detecting a risk of hypertension
XX by determining the pattern of alleles encoding a variant alpha-2B-
XX adrenoceptor (AR) protein. The methods and compositions of the invention
XX are useful for detecting risks and targeting treatment for hypertension.
XX The kit is also useful for selecting for clinical drug trials testing
XX the antihypertensive effect of compounds. The present sequence is human
XX alpha-2B-adrenoceptor gene.
XX
XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
SQ
Query Match 96.2%; Score 1302; DB 24; Length 1353;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGCCACAGAGACCCCTACTCCGTGACAGCCACAGCGGCATAGCGGCGCATCACC 60
Db 1 ATGAGCCACAGAGACCCCTACTCCGTGACAGCCACAGCGGCATAGCGGCGCATCACC 60

QY 61 TTCTCATTTCTCTTTACATCTTTCGCAACGCTGTGATCATCTGAGTGTGACACAGC 120
Db 61 TTCTCATTTCTCTTTACATCTTTCGCAACGCTGTGATCATCTGAGTGTGACACAGC 120
QY 121 CGCTGGCTGGGCCCCCTCAGAACTGTTCTGTGTGTGCTGTGGCGCGCCGACATCTTG 180
Db 121 CGCTGGCTGGGCCCCCTCAGAACTGTTCTGTGTGTGCTGTGGCGCGCCGACATCTTG 180
QY 181 GTGGCAGCGCTATCATCCCTTCTCGCTGGCCAAAGAGCTGTGGGCTACTGTATCTTC 240
Db 181 GTGGCAGCGCTATCATCCCTTCTCGCTGGCCAAAGAGCTGTGGGCTACTGTATCTTC 240
QY 241 CGGCGCAGCTGTGCGAGGTGTACCTGTGGCGCTGACGATGCTTCTTGCACCTGTTCATC 300
Db 241 CGGCGCAGCTGTGCGAGGTGTACCTGTGGCGCTGACGATGCTTCTTGCACCTGTTCATC 300
QY 301 GTGCACTGTGTGCGCATCAGCTGTGACCGCTACTGTGGCGGTGAGCCGCGCTGTGAGTAC 360
Db 301 GTGCACTGTGTGCGCATCAGCTGTGACCGCTACTGTGGCGGTGAGCCGCGCTGTGAGTAC 360
QY 361 AACTCCAGAGCGACCCCGCGCGCATCAAGTGCATCATCTGTGTGCTCATCTGCGC 420
Db 361 AACTCCAGAGCGACCCCGCGCGCATCAAGTGCATCATCTGTGTGCTCATCTGCGC 420
QY 421 GCGGTATCTGCTGCGCGCGCGCTCATCTTCAAGGCGACAGGCGCCCGCGCGCGG 480
Db 421 GCGGTATCTGCTGCGCGCGCGCTCATCTTCAAGGCGACAGGCGCCCGCGCGCGG 480
QY 481 CGCCCCAGTGAAGCTCAACAGAGGCTGTGTATCTGTGGCTTCCAGCATTCGAGATT 540
Db 481 CGCCCCAGTGAAGCTCAACAGAGGCTGTGTATCTGTGGCTTCCAGCATTCGAGATT 540
QY 541 TTCTTGTGCTTGTGCTCATCATGATCTGTGTCTACTGCGCATCATCTGTGCGCAAA 600
Db 541 TTCTTGTGCTTGTGCTCATCATGATCTGTGTCTACTGCGCATCATCTGTGCGCAAA 600
QY 601 CGCAGCAACCGCAGAGTCCAGAGGCGCAAGGCGGCGCTGTGGCAGAGTGTCAAGCAG 660
Db 601 CGCAGCAACCGCAGAGTCCAGAGGCGCAAGGCGGCGCTGTGGCAGAGTGTCAAGCAG 660
QY 661 CCCCAGACCCGACATGATGTGGGCTTTGGCTTCAGCAAACTGCGAGCTTGGCTCTGTG 720
Db 661 CCCCAGACCCGACATGATGTGGGCTTTGGCTTCAGCAAACTGCGAGCTTGGCTCTGTG 720
QY 721 GCTTGTGCAAGAGATGTAACGACATCTGAAAGTCCATGAGGAGAGAGAGGAGGAG 780
Db 721 GCTTGTGCAAGAGATGTAACGACATCTGAAAGTCCATGAGGAGAGAGAGGAGGAG 780
QY 781 ACCCTGAAAGATCTGGAGCCCGGCTTGGCCACCCAGTTGGGCTGCCCTTCCAACTCA 840
Db 781 ACCCTGAAAGATCTGGAGCCCGGCTTGGCCACCCAGTTGGGCTGCCCTTCCAACTCA 840
QY 841 GGCAGGGCCAGAGAGAGGAGGTTGTTGGGAGATCTCCAGAGATGAAGCTGAAGAGAG 900
Db 841 GGCAGGGCCAGAGAGAGGAGGTTGTTGGGAGATCTCCAGAGATGAAGCTGAAGAGAG 900
QY 901 GAAG 960
Db 901 GAAG 960
QY 961 TCAGTTGACAGCCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 TCAGTTGACAGCCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GGCAGAGTGTCTGTGGAG 1080
Db 1021 GGCAGAGTGTCTGTGGAG 1080
QY 1081 GCGAGAGTGAACCGGAG 1140
Db 1081 GCGAGAGTGAACCGGAG 1140
QY 1141 GTGCTGTGCTGTGCTTCTTCTTCAAGCTGTGAGCGGCGCATCTGCGCGAGAGAC 1200

|||||
 1141 GTGCTGTGCTGTCCCTTCTTCTTCTGAGCTACAGCTGGGCGCATCTGCGGAGAC 1200
 1201 TGAAGAGTGGCCATGAGCCCTTCCAGTCTTCTTGTGATGGCTACAGCAACACTCA 1260
 1201 TGAAGAGTGGCCATGAGCCCTTCCAGTCTTCTTGTGATGGCTACAGCAACACTCA 1260
 1261 CTGAACCTGTATCTTACACCATCTTCAACAGAGACTTCGCGCTGCTTCCGAGATC 1320
 1261 CTGAACCTGTATCTTACACCATCTTCAACAGAGACTTCGCGCTGCTTCCGAGATC 1320
 1321 CTGTGCGCGCCGTGAGACCAAGAGCGCTGCTGA 1353
 1321 CTGTGCGCGCCGTGAGACCAAGAGCGCTGCTGA 1353

RESULT 4
 ACAS6583
 ID ACAS6583 standard; cDNA; 2072 BP.

ACAS6583;
 06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1181.

Human; probe; ss; array element; Parkinson's disease;
 signalling pathway population; cancer; adenocarcinoma; leukaemia;
 immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens.

US6500938-B1.

31-DEC-2002.

30-JAN-1998; 98US-0016434.

30-JAN-1998; 98US-0016434.

(INCY-) INCYTE GENOMICS INC.

Au-Young J, Seilhamer JJ;

WPI; 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a
 microarray for monitoring the expression of a number of target
 polynucleotides -

Claim 1, SEQ ID NO 1181; 65pp; English.

The invention relates to a combination which, comprises a number of
 polynucleotide probes comprising a sequence selected from one of the 1490
 sequences mentioned in the specification. The combination is useful as an
 array element in a microarray for monitoring the expression of a number
 of target polynucleotides. The microarray is particularly useful in the
 diagnosis and treatment of cancer and immunopathology and neuropathology.
 The microarray is useful in diagnostics and treatment regimens, drug
 discovery and development, toxicological and carcinogenicity studies,
 forensics and pharmacogenomics. The microarray is also useful for
 monitoring progression of diseases and for developing sophisticated
 profiles for the effects of currently available therapeutic drugs. The
 combination is also useful for purifying a subpopulation of mRNA, cDNAs
 and genomic fragments and in research and diagnostic applications. The
 array can detect changes in expression in a large number of genes coding
 for different signalling pathway populations which can be used to diagnose
 various diseases including cancer e.g. adenocarcinoma and leukaemia;
 immunopathies e.g. AIDS and asthma; neuropathies e.g. Alzheimer's disease
 and Parkinson's disease. The present sequence represents a polynucleotide
 probe of the invention.
 Note: The sequence data for this patent did not form part of the printed
 specification but was obtained in electronic format directly from USPTO

CC at seqdata.uspto.gov/sequence.html?DocID=06500938B1.
 XX Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other;

Query Match 92.5%; Score 1251; DB 25; Length 2072;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGACACACAGAGACCCCTTCTTCTGAGGCGACAGGCGGACATGCGGCGCATCAC 60
 413 ATGAGACACACAGAGACCCCTTCTTCTGAGGCGACAGGCGGACATGCGGCGCATCAC 472
 61 TTCTCATTTCTCTTACATCTTCTGAGCAAGCTCTGATCTCTGCTGTGTTGACAC 120
 473 TTCTCATTTCTCTTACATCTTCTGAGCAAGCTCTGATCTCTGCTGTGTTGACAC 532
 121 CGCTGCTGCGGCGCCCTTCAAGAACTGTTCTGTGTGTGCTGCGCGCGCGCATCTG 180
 533 CGCTGCTGCGGCGCCCTTCAAGAACTGTTCTGTGTGTGCTGCGCGCGCGCATCTG 592
 181 GTGGCAGAGCTATCATCTCTTCTGCGGCGCAACAGCTGCTGAGCTTCTGCTTCT 240
 593 GTGGCAGAGCTATCATCTCTTCTGCGGCGCAACAGCTGCTGAGCTTCTGCTTCT 652
 241 CGGCGCAGCTGTGCGAGGTGTACCTGCGCTGACAGTCTCTTCTGCACTCTGCTCATC 300
 653 CGGCGCAGCTGTGCGAGGTGTACCTGCGCTGACAGTCTCTTCTGCACTCTGCTCATC 712
 301 GTGCACTGTGCGCATCAGCTGTGACCGCTTCTGAGCGGCGCTGAGCGCGCGCTGAGTAC 360
 713 GTGCACTGTGCGCATCAGCTGTGACCGCTTCTGAGCGGCGCTGAGCGCGCGCTGAGTAC 772
 361 AACTCAAGCGACCCCGCGCGCATCAGTGTATCTCTGAGTGTGCTGCTCATCTGCGC 420
 773 AACTCAAGCGACCCCGCGCGCATCAGTGTATCTCTGAGTGTGCTGCTCATCTGCGC 832
 421 GCCGTATCTGCTGCGCGCCCTTCTGCAAGAGGCGACAGGCGCGCGCGCGCGCG 480
 833 GCCGTATCTGCTGCGCGCCCTTCTGCAAGAGGCGACAGGCGCGCGCGCGCGCGCG 892
 481 CGGCGCAGTGTGCAAGCTCAACAGAGGCGCTGCTGATCTGCTGCTGCTGCTGCTGCT 540
 893 CGGCGCAGTGTGCAAGCTCAACAGAGGCGCTGCTGATCTGCTGCTGCTGCTGCTGCT 952
 541 TTCTTGTCTCTTCTGCTCATCTGATCTTGTCTTCTGCTGCTGCTGCTGCTGCTGCT 600
 953 TTCTTGTCTCTTCTGCTCATCTGATCTTGTCTTCTGCTGCTGCTGCTGCTGCTGCT 1012
 601 CGGAGCAACGAGAGGTCCAGAGGCGCAAGGCGGCGCTGCGAGGAGTGTGCAAGCAG 660
 1013 CGGAGCAACGAGAGGTCCAGAGGCGCAAGGCGGCGCTGCGAGGAGTGTGCAAGCAG 1072
 661 CCCGACCCGACCATGTGTGAGGCTTGTGCTGAGCCAACTGACGCTTGTGCTG 720
 1073 CCCGACCCGACCATGTGTGAGGCTTGTGCTGAGCCAACTGACGCTTGTGCTG 1132
 721 GCTTGTGCGAGAGGTCAACGACACTGAACTGCACTGCGGAGAGAGAGAGAGAGAG 780
 1133 GCTTGTGCGAGAGGTCAACGACACTGAACTGCACTGCGGAGAGAGAGAGAGAGAG 1192
 781 ACCCGTGAAGATATGTGGAGCCGCGGCTTGCACCAAGTGTGGAGTCTTCCCAACTCA 840
 1193 ACCCGTGAAGATATGTGGAGCCGCGGCTTGCACCAAGTGTGGAGTCTTCCCAACTCA 1252
 841 GCGCAGGCGCAGAGAGAGGTGTTGTGAGGATCTTCAAGAGATGAGCTGAAGAGAG 900
 1253 GCGCAGGCGCAGAGAGAGGTGTTGTGAGGATCTTCAAGAGATGAGCTGAAGAGAG 1312
 901 GAAAG 960
 1313 GAAAG 1372
 961 TCAGCTTGAGGCGCCCGCTGAGAGCAGAGGAGTCCGCGGAGTGTGCGACCCCTAAGT 1020

| | | | |
|----------|--|--|------|
| Qy | 601 | CGCAGCAACCGGAGAGGTCTCCAGGGCCAAAGGGGGGGCTTGGGCAAGGGTGAATCCAAAGCAG | 660 |
| Dp | 601 | CGCAGCAACCGGAGAGGTCTCCAGGGCCAAAGGGGGGGCTTGGGCAAGGGTGAATCCAAAGCAG | 660 |
| Qy | 661 | CCCCGACCCCGACCATAGTGTGGGGCTTTGGCCCTCAGCCAAACTCCAGCCCTGTGTG | 720 |
| Dp | 661 | CCCCGACCCCGACCATAGTGTGGGGCTTTGGCCCTCAGCCAAACTCCAGCCCTGTGTG | 720 |
| Qy | 721 | GCTTCTGCGCAAGAGAGTCAACGGACACTTCGAAGTCACTGGGGAGAGAGAGAGGGGGAG | 780 |
| Dp | 721 | GCTTCTGCGCAAGAGAGTCAACGGACACTTCGAAGTCACTGGGGAGAGAGAGAGGGGGAG | 780 |
| Qy | 781 | ACCCCTGAAGAATACCTGGGAGCCCGGGCCCTTGGCACCCAGTCATGTGGGGCTGGCCCTTCCCAACTCA | 840 |
| Dp | 781 | ACCCCTGAAGAATACCTGGGAGCCCGGGCCCTTGGCACCCAGTCATGTGGGGCTGGCCCTTCCCAACTCA | 840 |
| Qy | 841 | GGCCAGGGCCAGAAAGAGAGGGTGTTTGTGTGGGCAATCTCCAGAGAGATGAAGCTGAAGAGAG | 900 |
| Dp | 841 | GGCCAGGGCCAGAAAGAGAGGGTGTTTGTGTGGGCAATCTCCAGAGAGATGAAGCTGAAGAGAG | 900 |
| Qy | 901 | GAAGAGAGAGAGAGAGAGAGAGAGAGAGTGTGAATCCCAAGGCAGTGCACATGTCTTCGGGCC | 960 |
| Dp | 901 | GAAGAGAGAGAGAGAGAGAGAGAGAGAGTGTGAATCCCAAGGCAGTGCACATGTCTTCGGGCC | 960 |
| Qy | 961 | TCAGCTTGCAACCCCCCGCTGCGACAGACGCAACAGGGCTCCCGGGTCTGGCCACCTTAAGT | 1020 |
| Dp | 961 | TCAGCTTGCAACCCCCCGCTGCGACAGACGCAACAGGGCTCCCGGGTCTGGCCACCTTAAGT | 1020 |
| Qy | 1021 | GGCCAGGTGCTCTTGGGAGAGGGGCGTGGGTGCTATAAGGTGGGCAATGTGGCGGTGCAAGG | 1080 |
| Dp | 1021 | GGCCAGGTGCTCTTGGGAGAGGGGCGTGGGTGCTATAAGGTGGGCAATGTGGCGGTGCAAGG | 1080 |
| Qy | 1081 | GGCGCAGCTGACCCCGGAGAAAGCGCTTCACTTCGTGCTGGCTGAGTCAATTGGCGTTTTT | 1140 |
| Dp | 1081 | GGCGCAGCTGACCCCGGAGAAAGCGCTTCACTTCGTGCTGGCTGAGTCAATTGGCGTTTTT | 1140 |
| Qy | 1141 | GTCGCTCTGCTGGTTCCCTCTTCTTCTTCAAGCTACAGCTGGGGCGCATCTGGCCGGAAGAC | 1200 |
| Dp | 1141 | GTCGCTCTGCTGGTTCCCTCTTCTTCTTCAAGCTACAGCTGGGGCGCATCTGGCCGGAAGAC | 1200 |
| Qy | 1201 | TGCAAGAGTGGCCCATGAGGCTCTTCCAGTTCTTCTTGTGAGATCGGCTACATGCAACAGCTCA | 1260 |
| Dp | 1201 | TGCAAGAGTGGCCCATGAGGCTCTTCCAGTTCTTCTTGTGAGATCGGCTACATGCAACAGCTCA | 1260 |
| Qy | 1261 | CTGAACCTGTATTATCTACACCATCTTCAACAGAGATTCCGCGGTGCTTCGAGAGATC | 1320 |
| Dp | 1261 | CTGAACCTGTATTATCTACACCATCTTCAACAGAGATTCCGCGGTGCTTCGAGAGATC | 1320 |
| Qy | 1321 | CTGTGCGCGCCGTGAGACCCAGACGGCGCTGTGTA | 1353 |
| Dp | 1321 | CTGTGCGCGCCGTGAGACCCAGACGGCGCTGTGTA | 1353 |
| RESULT 6 | | | |
| AAD04761 | | | |
| ID | AAD04761 standard; DNA; 1344 BP. | | |
| XX | AAD04761; | | |
| DT | 04-JUL-2001 (first entry) | | |
| DE | Human alpha2B-adrenoceptor (alpha2B-AR) variant gene. | | |
| KW | Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; | | |
| KW | glutamic acid repeat; intracellular loop; chromosome 2; catecholamine; | | |
| KW | norepinephrine; epinephrine; therapy; vascular contraction; variant; | | |
| KW | coronary artery; coronary heart disease; CHD; chronic angina pectoris; | | |
| XX | acute myocardial infarction; AMI; Primizmetals variant; ds. | | |
| OS | Homo sapiens. | | |
| Key | Location/Qualifiers | | |
| FT | 1..1344 | | |

| | |
|---------------------------|---|
| FT | /tag= a |
| PT | /product= "Human alpha2B-adrenoceptor (alpha2B-AR) |
| ET | variant protein" |
| FN | |
| PN | WO200129082-A1. |
| PD | 26-APR-2001. |
| XX | |
| PF | 20-OCT-2000; 2000MO-FI00913. |
| XX | |
| PR | 22-OCT-1999; 99US-0422985. |
| PA | (JUVVA-) JUVANTIA PHARMA LTD OY. |
| P1 | Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U; |
| P1 | Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Mylssönen K; |
| P1 | Salonen R, Kahkonen J, Valkonen V; |
| DR | WPI; 2001-300318/31. |
| XX | |
| DR | P-PSTDB; NAE00989. |
| XX | |
| PT | New DNA molecule encoding variant specific adrenoceptor protein with |
| PT | deletion of specific amino acids located in the third intracellular |
| PT | loop of the polypeptide, for treating vascular contraction of coronary |
| PT | arteries - |
| PS | Claim 3; Page 24-26; 37pp; English. |
| CC | The present sequence is a gene encoding human alpha2B-adrenoceptor |
| CC | (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat |
| CC | element (amino acids 298-309) of 12 glutamates, in an acidic stretch of |
| CC | 18 amino acids (amino acids 294-311), located in the third intracellular |
| CC | loop of the receptor polypeptide. The variant is obtained by deletion of |
| CC | three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR |
| CC | gene is located on chromosome 2. Alpha2-AR mediate many of the |
| CC | physiological effects of the catecholamines, norepinephrine and |
| CC | epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating |
| CC | a mammal suffering from vascular contraction of coronary arteries and a |
| CC | disease involving vascular contraction of coronary arteries which is |
| CC | clinically expressed as coronary heart disease (CHD), unstable chronic |
| CC | angina pectoris which is clinically expressed as Prinzmetal's variant |
| CC | form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in |
| CC | gene therapy. |
| XQ | |
| SQ | Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other; |
| Query Match | 67.8%; Score 918; DB 22; Length 1344; |
| Blast Local Similarity | 100.0%; Pred. No. 0; |
| Matches 918; Conservative | 0; Mismatches 0; Indels 0; Gaps 0 |
| OY | 1 ATGAGCACAACGAAGCCCCTACTCGGTGCAGGCCAAGGGCCATAGCGGCCCATCAC |
| Db | 1 ATGAGCACAACGAAGCCCCCTACTCGGTGCAGGCCAAGGGCCATAGCGGCCCATCAC |
| OY | 61 TTCTCAATTCTTTTACCATCTTGAGCAAGCTCTGTGCATTCCTGGCTGTGTACACAGC |
| Db | 61 TTCCTCAATTCTTTTACCATCTTGAGCAAGCTCTGTGCATTCCTGGCTGTGTACACAGC |
| OY | 121 CGCTCGCGGGGGGGCCCTCAGAAGCTGTTCCTGGTGTGGCGCGCGCGGCACATCCMG |
| Db | 121 CGCTCGCGGGGGGGCCCTCAGAAGCTGTTCCTGGTGTGGCGCGCGCGGCACATCCMG |
| OY | 181 GTGGCGACGCTCANCATCCCTTTCCTCGCTGGCGAACAGAGCTGGGCTACTGTGTAATTC |
| Db | 181 GTGGCGACGCTCANCATCCCTTTCCTCGCTGGCGAACAGAGCTGGGCTACTGTGTAATTC |
| OY | 241 CGGCGACGCTGTGAGGTGTACTCTGGCGCTCGACGCTCTTCTTGACCTCGTTCATC |
| Db | 241 CGGCGACGCTGTGAGGTGTACTCTGGCGCTCGACGCTCTTCTTGACCTCGTTCATC |
| OY | 301 GTGACACCTGTGGCCATAGCGCTGAGCGGCTACCTGGGCGGTGAGCGGGCGTGGAGTAC |
| Db | 301 GTGACACCTGTGGCCATAGCGCTGAGCGGCTACCTGGGCGGTGAGCGGGCGTGGAGTAC |
| OY | 360 GTGACACCTGTGGCCATAGCGCTGAGCGGCTACCTGGGCGGTGAGCGGGCGTGGAGTAC |
| Db | 360 GTGACACCTGTGGCCATAGCGCTGAGCGGCTACCTGGGCGGTGAGCGGGCGTGGAGTAC |

| | |
|---------------------------|--|
| PI | Salonen J; |
| XX | WPI; 2002-667063/71. |
| DR | P-PSDB; AAE26633. |
| PT | Detecting a risk of hypertension and targeting treatment in a subject |
| PR | by determining the pattern of alleles encoding a variant |
| PT | alpha-2-adrenoceptor - |
| XX | |
| PS | Disclosure, Page 24-26; 35pp; English. |
| CC | The invention relates to a method for detecting a risk of hypertension |
| CC | by determining the pattern of alleles encoding a variant alpha-2B- |
| CC | adrenoceptor (AR) protein. The methods and compositions of the invention |
| CC | are useful for detecting risks and targeting treatment for hypertension. |
| CC | The kit is also useful for selecting for clinical drug trials testing |
| CC | the antihypertensive effect of compounds. The present sequence is human |
| CC | alpha-2B-adrenoceptor variant DNA. |
| SQ | |
| SQ | Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other; |
| Query Match | 67.8%; Score 918; DB 24; Length 1344; |
| Best Local Similarity | 100.0%; Pred. No. 0; |
| Matches 918; Conservative | 0; Mismatches 0; Indels 0; Gaps 0 |
| OY | 1 ATGGAGCAACGAGAGCCCTACTCGGTGAGGCCAAGCGGCATGCGGCATCAC |
| Db | 1 ATGGAGCAACGAGAGCCCTACTCGGTGAGGCCAAGCGGCATGCGGCATCAC |
| OY | 61 TTCCTCATCTTCTTTAACCATCTTGCGGAACGCTGTGTCATCTGGCTGTGGACAGC |
| Db | 61 TTCCTCATCTTCTTTAACCATCTTGCGGAACGCTGTGTCATCTGGCTGTGGACAGC |
| OY | 121 CGCTGCTGCGCGCCCTCAGAACTGTTCCGGGTGTGCTGGCCCGCCGCGAAGATCTTG |
| Db | 121 CGCTGCTGCGCGCCCTCAGAACTGTTCCGGGTGTGCTGGCCCGCCGCGAAGATCTTG |
| OY | 181 GTGGCCACGCTTCATCATCTCTTCTCGGTGCGCAAAGAGCTGTGGCTACTGTGATCTTC |
| Db | 181 GTGGCCACGCTTCATCATCTCTTCTCGGTGCGCAAAGAGCTGTGGCTACTGTGATCTTC |
| OY | 241 CGGCGCAGTGTGTGAGGTGTACCTGGCGGTGCAACGTCGCTCTTGTGCACTCGTTCATC |
| Db | 241 CGGCGCAGTGTGTGAGGTGTACCTGGCGGTGCAACGTCGCTCTTGTGCACTCGTTCATC |
| OY | 301 GTGCACCTGTGCGGCATCAGCGCTGAGACCGCTACTAGGGCCGTGAGACCGCGCGCTGAGTAC |
| Db | 301 GTGCACCTGTGCGGCATCAGCGCTGAGACCGCTACTAGGGCCGTGAGACCGCGCGCTGAGTAC |
| OY | 361 AAATTCCAAGCGCACCCTGGCGGCGCATCAAGTGCATCATCTCACTGTGTGGCTCATGCCC |
| Db | 361 AAATTCCAAGCGCACCCTGGCGGCGCATCAAGTGCATCATCTCACTGTGTGGCTCATGCCC |
| OY | 421 GCCTGTCACTGTGCTGCGCGCCCTCATCATCAAGAAGGCGAACCGAGGCGCGCGGG |
| Db | 421 GCCTGTCACTGTGCTGCGCGCCCTCATCATCAAGAAGGCGAACCGAGGCGCGCGGG |
| OY | 481 CGCCCCAAGTGCAGAGCTTCAACGAGAGGCGCTGTATCTCTGGCTTCAGATCGATCT |
| Db | 481 CGCCCCAAGTGCAGAGCTTCAACGAGAGGCGCTGTATCTCTGGCTTCAGATCGATCT |
| OY | 541 TTCTTTGCTCTGTCCTCATCATGATCTCTGTCTCACTGTGGCATCTACCTGATCGCAAA |
| Db | 541 TTCTTTGCTCTGTCCTCATCATGATCTCTGTCTCACTGTGGCATCTACCTGATCGCAAA |
| OY | 601 CGAGCAACCGCAGAGGTCCAGAGGCGCAAGGAGGCGCTGTGGAGGTGAGTCCAAAGAG |
| Db | 601 CGAGCAACCGCAGAGGTCCAGAGGCGCAAGGAGGCGCTGTGGAGGTGAGTCCAAAGAG |
| OY | 661 CCCGAGACCGACCATGATGTGGGGCTTTGGCTTCAGCCAAATGTCGACCTCTGCTGTG |
| Db | 661 CCCGAGACCGACCATGATGTGGGGCTTTGGCTTCAGCCAAATGTCGACCTCTGCTGTG |

QY 721 GCTTCTGCCAGAGAGTCAACGACACTCGAAGTCCACTGGGAGAGAGAGGAGGAG 780
DB 721 GCTTCTGCCAGAGAGTCAACGACACTCGAAGTCCACTGGGAGAGAGAGGAGGAG 780
QY 781 ACCCTGAAAGATCTGGGACCCCGGCTTGCACCAAGTTGGGCTCCCTTCCCACTCA 840
DB 781 ACCCTGAAAGATCTGGGACCCCGGCTTGCACCAAGTTGGGCTCCCTTCCCACTCA 840
QY 841 GGCAGAGGCGAGAGAGGAGTGTGTGTGGGCGATCTCCAGAGATGAGCTGAAGAGAG 900
DB 841 GGCAGAGGCGAGAGAGGAGTGTGTGTGGGCGATCTCCAGAGATGAGCTGAAGAGAG 900
QY 901 GAAAGAGAGAGAGAGAG 918
DB 901 GAAAGAGAGAGAGAGAG 918

RESULT 8
AA199906
ID AA199906 standard; DNA; 1344 BP.
XX
AC AA199906;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; db.
XX
OS Homo sapiens.

Key Location/Qualifiers
FH 1..1344
FT /tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence is deleted for a 9 nucleotide
polymorphic site found at nucleotides 901-909
of the wildtype alpha-2BAR protein (AA199905)"
FT
PN MO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001MO-US12575.
XX
PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52118.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
PS Claim 5; Page 144-145; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909

CC of (I), a site comprising cytosine or guanine at position 753 of (II)
CC or a site comprising (A) (ggggcggggcgc) or (B) (ggggcggcgcag) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2C, comprising detecting a
CC polymorphic site which correlates to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfscine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
CC polymorphic site found at nucleotides 901-909 of the wildtype gene
CC (AA199905).
XX
SQ Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;
XX
Query Match 66.7%; Score 902; DB 23; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGACACCAAG 60
DB 1 ATGACACCAAG 60
QY 61 TTCTCATTTCTCTTACATCTTGGCAAGCTCTGATATCTGCTGTGTTGACACAG 120
DB 61 TTCTCATTTCTCTTACATCTTGGCAAGCTCTGATATCTGCTGTGTTGACACAG 120
QY 121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCTGTGTGCTGCTGCGCGCCGACATCTTG 180
DB 121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCTGTGTGCTGCTGCGCGCCGACATCTTG 180
QY 181 GTGGCAGCCTCATCATCTCTTCTGCTGCGCAAGAGCTGTGGGCTACTGTGTTTC 240
DB 181 GTGGCAGCCTCATCATCTCTTCTGCTGCGCAAGAGCTGTGGGCTACTGTGTTTC 240
QY 241 CGGCGAGGTGGAGAGGTGATACCTGCGGCTCGACGTCTCTTGACACTCGTCCATC 300
DB 241 CGGCGAGGTGGAGAGGTGATACCTGCGGCTCGACGTCTCTTGACACTCGTCCATC 300
QY 301 GTGCACTGTGCGCATCAGCTGTGACCGCTACTGAGCGCGCGCTGAGTAC 360
DB 301 GTGCACTGTGCGCATCAGCTGTGACCGCTACTGAGCGCGCGCTGAGTAC 360
QY 361 AACTCAGAGCGAG 420
DB 361 AACTCAGAGCGAG 420
QY 421 GCGTCATCTGCTGCGCGCCCTCATCTCAAGAGCGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GCGTCATCTGCTGCGCGCCCTCATCTCAAGAGCGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 CGCAG 540
DB 481 CGCAG 540
QY 541 TTCTTTGCTCTGCTGCTCATCATGATCTTGTCTACCTGCGAGATCTACTGAGCAAA 600
DB 541 TTCTTTGCTCTGCTGCTCATCATGATCTTGTCTACCTGCGAGATCTACTGAGCAAA 600
QY 601 CGCAG 660
DB 601 CGCAG 660
QY 661 CCCGAG 720
DB 661 CCCGAG 720

Db 661 CCCCGACCCGACATGATGAGGCTTTGAGCTTCAGCCAACTGCGAGCCCTGAGCTTGTG 720
QY 721 GCTTCTCCAGAGAGGTCAACGAGCACTGAAAGTCACTGAGGAGAGAGAGGAGGAG 780
Db 721 GCTTCTCCAGAGAGGTCAACGAGCACTGAAAGTCACTGAGGAGAGAGAGGAGGAG 780
QY 781 ACCCTGAAGATPACTGAGAGCCCGGCTTTCAGCCAGTTGGCTGCTTTCAGACTCA 840
Db 781 ACCCTGAAGATPACTGAGAGCCCGGCTTTCAGCCAGTTGGCTGCTTTCAGACTCA 840
QY 841 GGGCAGGAGCCAGAGAGGAGGTTTGTGGGAGCATCTCAGAGAGTGAAGCTGAAGAGAG 900
Db 841 GGGCAGGAGCCAGAGAGGAGGTTTGTGGGAGCATCTCAGAGAGTGAAGCTGAAGAGAG 900
QY 901 GA 902
Db 901 GA 902
Db 901 GA 902

RESULT 9

AAQ14151 standard; DNA: 2064 BP.

XX AAQ14151;
XX AC
XX AAQ14151;
XX 06-JAN-1992 (first entry)
XX 06-JAN-1992 (first entry)
XX Human alpha 2 beta adrenergic receptor gene.
XX Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
XX Homo. sapiens.
XX OS
XX Key Location/Qualifiers
XX FT CDS 288..1752
XX FT /*tag= a
XX FT
XX US5053337-A.
XX PN 01-OCT-1991.
XX PD 01-OCT-1991.
XX PF 30-OCT-1989; 89US-0428856.
XX PR 30-OCT-1989; 89US-0428856.
XX PA (NEUR-) NEUROGENETIC CORP.
XX PI Weishank RL, Hartig PR;
XX DR WPI, 1991-310087/42.
XX DR P-PSDB; AARI1419.
XX PT Isolated DNA encoding human adrenergic receptor - for detecting
XX PT nucleic acids encoding alpha, 2-beta adrenergic receptor, for
XX PT screening drugs.
XX PS Claim 1, Fig 2, 15pp; English.
XX CC Clone NGC-alpha2beta was isolated from a human spleen genomic
XX CC library by screening with a fragment of the human 5-HT1A receptor
XX CC gene. The gene can be used to express recombinant receptor protein
XX CC which can be used to produce antibodies for inhibition of receptor
XX CC function.
XX SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;

Query Match 60.6%; Score 820; DB 12; Length 2064;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 970; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 381 CCGCATCAAGTGCATATCTCTCACTGTGTGCTCATCGCCGCGCATCTGCTGCGCC 440
Db 779 CCGCATCAAGTGCATATCTCTCACTGTGTGCTCATCGCCGCGCATCTGCTGCGCC 838

QY 441 CTTATCTCAAGAGGAGCAAGAGGAGCCCGAGCCGCGGAGCCCGCCAGTGCAGACTCA 500
Db 839 CTTATCTCAAGAGGAGCAAGAGGAGCCCGAGCCCGGAGCCCGCCAGTGCAGACTCA 898
QY 501 CCAAGAGGCTGTGTACATCTGTGCTTCAGAGATCTTTTCTTTGCTCTTGTGCTCAT 560
Db 899 CCAAGAGGCTGTGTACATCTGTGCTTCAGAGATCTTTTCTTTGCTCTTGTGCTCAT 958
QY 561 CATGATCTTGTCTTACTGCTGAGCATCTTACCTGATGCGCAAGAGAGAGAGAGAGTCC 620
Db 959 CATGATCTTGTCTTACTGCTGAGCATCTTACCTGATGCGCAAGAGAGAGAGAGTCC 1018
QY 621 CAGGAGCAAGAGGAGGAGCTGTGAGAGAGTGAAGTCAAGAGAGAGAGAGAGAGAGTCC 680
Db 1019 CAGGAGCAAGAGGAGGAGCTGTGAGAGAGTGAAGTCAAGAGAGAGAGAGAGAGTCC 1078
QY 681 GGGTTTGGCTTCAAGCAATCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCAA 740
Db 1079 GGGTTTGGCTTCAAGCAATCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCAA 1138
QY 741 CCGAATCTTCAAGAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCAAG 800
Db 1139 CCGAATCTTCAAGAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTCAAG 1198
QY 801 CCGGAGCTTGTGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 860
Db 1199 CCGGAGCTTGTGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1258
QY 861 TGTGTTGAGGAGCATCTTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 920
Db 1259 TGTGTTGAGGAGCATCTTCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1318
QY 921 GGAAGAGTGAAG 980
Db 1319 GGAAGAGTGAAG 1378
QY 981 GCAAGAGCAAG 1040
Db 1379 GCAAGAGCAAG 1438
QY 1041 GGGGCTGAGGAGTATAG 1100
Db 1439 GGGGCTGAGGAGTATAG 1498
QY 1101 GCGCTTCACTTCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1160
Db 1499 GCGCTTCACTTCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1558
QY 1161 CTTTCTCACTTCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1220
Db 1559 CTTTCTCACTTCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1618
QY 1221 CTTTCACTTCTTCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1280
Db 1619 CTTTCACTTCTTCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1678
QY 1281 CATCTTCAACAGAGACTTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1340
Db 1679 CATCTTCAACAGAGACTTCCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1738
QY 1341 GAGGAGCTGTGTA 1353
Db 1739 GAGGAGCTGTGTA 1751

RESULT 10

AAT59499 standard; DNA: 2064 BP.

XX AAT59499;
XX AC
XX AAT59499;
XX 25-MAR-2003 (updated)

DT 06-MAY-1997 (first entry)
XX Human alpha-2b adrenergic receptor genomic DNA clone.
DE Alpha-2b adrenergic receptor; adrenoreceptor; adrenaline;
XX epinephrine; signal transduction; neurotransmitter; ligand; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 288..1751
FT /-tag= a
XX
XX US595880-A.
XX
XX 21-JAN-1997.
XX
XX 22-OCT-1992; 92US-0965040.
XX
XX 30-OCT-1989; 89US-0428856.
XX 30-MAY-1991; 91US-0707604.
XX 22-OCT-1992; 92US-0965040.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX Hartig PR, Weisshank RL;
XX
XX WPI: 1997-107576/10.
XX P-PSDB; AAW11804.
XX
XX Assay for alpha-2b adrenergic receptor ligands - using membranes of
XX cells expressing recombinant receptor
XX
XX Disclosure; Fig 2A-E; 16pp; English.
XX
XX A genomic DNA clone (AA159499) codes for human alpha-2b adrenergic
XX receptor (AAW11804), a member of the rhodopsin-like signal transducer
XX family. It was isolated from a human spleen genomic library in the
XX lambda vector Charon 28 by screening with a 1.6 kb fragment of the
XX human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2b
XX comprising DNA encoding the alpha-2b adrenoreceptor is deposited as
XX ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2b
XX adrenoreceptor in bacterial, yeast or mammalian cells; transfected
XX Ltk- cells, designated L-NGC-alpha-2b, are deposited as ATCC CRL
XX 10275. Membranes of such cells can used in novel methods to
XX identify drugs which specifically interact with, and bind to, the
XX alpha-2b adrenergic receptor.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
SQ
Query Match 60.6%; Score 820; DB 18; Length 2064;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 381 CGGCATCAAGTGCATCTCACTGCTGCTCATCGCGCGCTCATCTCGTGGCGCC 440
DB 779 CCGCATCAAGTGCATCTCACTGCTGCTCATCGCGCGCTCATCTCGTGGCGCC 838
QY 441 CCTCATCTCAAGGCGACGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 500
DB 839 CCTCATCTCAAGGCGACGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 898
QY 501 CCAAGAGGCGCTGTACATCTGTGCTTCAGCATCGGATCTTTTGTCTCTTGTCTCAT 560
DB 899 CCAAGAGGCGCTGTACATCTGTGCTTCAGCATCGGATCTTTTGTCTCTTGTCTCAT 958
QY 561 CATGATCTTGTCTACCTGCGCATCTACCTGATCGCAAGCAAGCAAGCAAGCAAGTCC 620
DB 959 CATGATCTTGTCTACCTGCGCATCTACCTGATCGCAAGCAAGCAAGCAAGCAAGTCC 1018
QY 621 CAGGCGCAAGGAGGCGCTGTGCGAGGTGATCCAGCAAGCCCGCAAGCATGATG 680

DB 1019 CAGGCGCAAGGAGGCGCTGTGCGAGGTGATCCAGCAAGCCCGCAAGCATGATG 1078
QY 681 GCGTTTGCCCTCAGCAAGTCCAGCGCTGCGCTCTGTGCTTCTGCCAGAGAGGTCAA 740
DB 1079 GCGTTTGCCCTCAGCAAGTCCAGCGCTGCGCTCTGTGCTTCTGCCAGAGAGGTCAA 1138
QY 741 CCGACACTGAAAGTCCATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 800
DB 1139 CCGACACTGAAAGTCCATCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
QY 801 CCGGCGCTTGCCAGCAAGTGGCTGCTGCTTCCCACTAGAGCAGAGGCAAGAGAGG 860
DB 1199 CCGGCGCTTGCCAGCAAGTGGCTGCTGCTTCCCACTAGAGCAGAGGCAAGAGAGG 1258
QY 861 TGTGTGGGGGATCTCCAGAGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 920
DB 1259 TGTGTGGGGGATCTCCAGAGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1318
QY 921 GGAAGAGTGAACCCAG 980
DB 1319 GGAAGAGTGAACCCAG 1378
QY 981 GCAAGAGCAAGAGGCTCCCGGCTGCGCACACCTTACGTGCGAGGTCTCTGGGAG 1040
DB 1379 GCAAGAGCAAGAGGCTCCCGGCTGCGCACACCTTACGTGCGAGGTCTCTGGGAG 1438
QY 1041 GGGCGTGGGTGCTATAGTGGGAGAGTGGGAGTGGAGAGAGAGAGAGAGAGAGAG 1100
DB 1439 GGGCGTGGGTGCTATAGTGGGAGAGTGGGAGTGGAGAGAGAGAGAGAGAGAGAG 1498
QY 1101 GGGCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160
DB 1499 GGGCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1558
QY 1161 CTTCTTCACTTCAAGCTGCGCGCATCTGCGCGCAAGCAAGTCCAGAGTCCCATG 1220
DB 1559 CTTCTTCACTTCAAGCTGCGCGCATCTGCGCGCAAGCAAGTCCCATGAGGCT 1618
QY 1221 CTTTCAAGTCTTCTTGTGATGCGCTACCTGCAAGCTTCAAGTCCCTGTTATCTAC 1280
DB 1619 CTTTCAAGTCTTCTTGTGATGCGCTACCTGCAAGCTTCAAGTCCCTGTTATCTAC 1678
QY 1281 CATCTTCAACAGAGCTTCCGCGCTTCCGAGAGATCTGTGCGCGCGCGCGCGCGCA 1340
DB 1679 CATCTTCAACAGAGCTTCCGCGCTTCCGAGAGATCTGTGCGCGCGCGCGCGCGCA 1738
QY 1341 GACGCGCTGTGA 1353
DB 1739 GACGCGCTGTGA 1751
RESULT 11
ABN32100
ID ABN32100 standard; DNA; 65 BP.
XX
XX ABN32100;
XX
XX 15-JUL-2002 (first entry)
XX
XX Rat spliced transcript detection oligonucleotide SEQ ID NO:4848.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Rattus norvegicus.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-1B01903.
XX
XX 28-JUL-2000; 2000US-221607P.
XX


```

FH Key Location/Qualifiers
FT CDS 1..1353
FT /*tag= a
FT /*product= "alpha-2AAR"
XX
XX WO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12575.
XX
XX 17-APR-2000; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
XX (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI: 2001-611728/70.
XX P-PSDB; AAMS2122.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX Example 7; Page 151; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX alpha2A or alpha2C or fragment or complement of; and
XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX of (I), a site comprising cytosine or guanine at position 753 of (IIV)
XX or a site comprising (A) (999GCG99GCG) or (B) (999GCGCTGAG) at
XX positions 961-972 of (III). The method may be used for genotyping an
XX alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX whether an individual is at increased risk of developing a disease
XX associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX polymorphic site which correlate to disease selected from cardiovascular
XX disease, central nervous system disease and combinations of these. In
XX addition, the technique may be used to predict an individual's response
XX to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, BHT933 and
XX norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX rauwolfine, idazoxan, tolazoline, phentolamine and combinations of
XX these) by detecting the polymorphic site and correlating the site to a
XX predetermined response (where the response is correlated to adenylyl
XX cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX levels). The present sequence is that of the human alpha-2AAR gene
XX (Genbank Accession AF281308).
XX
XX Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
XX
XX Query Match 3.3%; Score 45; DB 23; Length 1350;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-10;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 292 TCGTCATCGTGCACCTGTGCGCATCAGCTGACCGCTACTG 336
XX |||||||||||||||||||||||||||||||||||||||
XX Db 355 TCGTCATCGTGCACCTGTGCGCATCAGCTGACCGCTACTG 399
XX
XX RESULT 14
XX AA199918
XX ID AA199918 standard; DNA; 1350 BP.
XX AC AA199918;
XX XX
XX 18-FEB-2002 (first entry)
XX
```

```

DE Human alpha-2AAR variant encoding DNA.
XX
XX Human: genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polymorphic site; allelic variant; cardiovascular disease;
XX central nervous system disease; adenylyl cyclase; MAP kinase activity;
XX phosphorylation; inositol phosphate; alpha-2AAR; chromosome 10; db.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1353
XX /*tag= a
XX /*product= "alpha-2AAR"
XX /*replace(753,C)
XX /*tag= b
XX
XX WO200179561-A2.
XX
XX 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12575.
XX
XX 17-APR-2000; 2000US-0551744.
XX 10-AUG-2000; 2000US-0636259.
XX 19-OCT-2000; 2000US-0692077.
XX
XX (LIGG/) LIGGETT S B.
XX (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
XX WPI: 2001-611728/70.
XX P-PSDB; AAMS2123.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
XX determining whether an individual is at increased risk of developing a
XX disease associated with the corresponding receptor comprises detecting
XX a polymorphic site -
XX
XX disclosure; Page 152; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
XX receptor gene (I)-(III) by detecting a polymorphic site, comprising:
XX (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
XX alpha2A or alpha2C or fragment or complement of; and
XX (b) detecting a polymorphic site comprising nucleotide positions 901-909
XX of (I), a site comprising cytosine or guanine at position 753 of (IIV)
XX or a site comprising (A) (999GCG99GCG) or (B) (999GCGCTGAG) at
XX positions 961-972 of (III). The method may be used for genotyping an
XX alpha2B, alpha2A or alpha2C receptor gene and further used to determine
XX whether an individual is at increased risk of developing a disease
XX associated with alpha2B, alpha2A or alpha2, comprising detecting a
XX polymorphic site which correlate to disease selected from cardiovascular
XX disease, central nervous system disease and combinations of these. In
XX addition, the technique may be used to predict an individual's response
XX to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
XX norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
XX combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
XX rauwolfine, idazoxan, tolazoline, phentolamine and combinations of
XX these) by detecting the polymorphic site and correlating the site to a
XX predetermined response (where the response is correlated to adenylyl
XX cyclase, MAP kinase activity, phosphorylation or inositol phosphate
XX levels). The present sequence is that of the human alpha-2AAR variant
XX gene.
XX
XX Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;
XX
XX Query Match 3.3%; Score 45; DB 23; Length 1350;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-10;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 292 TCGTCATCGTGCACCTGTGCGCATCAGCTGACCGCTACTG 336
XX |||||||||||||||||||||||||||||||||||||||
XX
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Db 355 TCGTCATGTCGACCTGTGGCCATCAGCTGACCGCTACTGG 399

Search completed: February 8, 2004, 01:59:37
Job time : 402.321 secs

RESULT 15

ACAS6582
ID ACAS6582 standard; cDNA; 3604 BP.

AC ACAS6582;

DT 06-JUN-2003 (first entry)

DE Human signalling pathway polynucleotide probe SEQ ID NO 1180.

KW Human; Probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

OS Homo sapiens.

PN US6500938-B1.

PD 31-DEC-2002.

PF 30-JAN-1998; 98US-0016434.

PR 30-JAN-1998; 98US-0016434.

PA (INCY-) INCYTE GENOMICS INC.

PI Au-Young J, Sellhammer JU;

DR WPI; 2003-352169/33.

PT Combination of polynucleotide probes, useful as array elements in a

PT microarray for monitoring the expression of a number of target

PT polynucleotides -

PS Claim 1; SEQ ID NO 1180; 65pp; English.

CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostic and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signalling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docID=06500938B1.

XX Sequence 3604 BP; 555 A; 1272 C; 1134 G; 643 T; 0 other;

Query Match 3.3%; Score 45; DB 25; Length 3604;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 292 TCGTCATGTCGACCTGTGGCCATCAGCTGACCGCTACTGG 336

Db 2432 TCGTCATGTCGACCTGTGGCCATCAGCTGACCGCTACTGG 2476

QY 601 CGCAGCAACCGAGAGTCCAGAGGCGCAAGGGGGGCGCTTGAGGAGGGTGTCAAGCAG 660
DB 1013 CGCAGCAACCGAGAGTCCAGAGGCGCAAGGGGGGCGCTTGAGGAGGGTGTCAAGCAG 1072
QY 661 CCCCCGACCCGACCATGATGGGGGCTTTGGCTTCAGCCAACTGCGACCCCTTGCTGTG 720
DB 1073 CCCCCGACCCGACCATGATGGGGGCTTTGGCTTCAGCCAACTGCGACCCCTTGCTGTG 1132
QY 721 GCTTCTGCCAGAGAGTCAACGCACTGGAAGTCACTGAGGAGGAAGAGAGGAGGAG 780
DB 1133 GCTTCTGCCAGAGAGTCAACGCACTGGAAGTCACTGAGGAGGAAGAGAGGAGGAG 1192
QY 781 ACCCTGAGAGTACTGAGGACCCGAGGCTTGCAACCGAGTTGAGCTCCCTTCCCACTCA 840
DB 1193 ACCCTGAGAGTACTGAGGACCCGAGGCTTGCAACCGAGTTGAGCTCCCTTCCCACTCA 1252
QY 841 GGCAGAGGCGCAAGAGAGGGGTGTTGTGGGCACTTCCAGAGATGAAGTGAAGAGAG 900
DB 1253 GGCAGAGGCGCAAGAGAGGGGTGTTGTGGGCACTTCCAGAGATGAAGTGAAGAGAG 1312
QY 901 GAAG 960
DB 1313 GAAG 1372
QY 961 TCAGCTTGACAGCCCGCTGACAGACAGAGAGCTCCGAGTGTGAGCACTTACGT 1020
DB 1373 TCAGCTTGACAGCCCGCTGACAGACAGAGAGCTCCGAGTGTGAGCACTTACGT 1432
QY 1021 GGCAGAGTGTCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1433 GGCAGAGTGTCTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1492
QY 1081 GCGCAGCTGACCCGAG 1140
DB 1493 GCGCAGCTGACCCGAG 1552
QY 1141 GTGCTGTGAGTGTCCCTCTTCTTCTGAGTACAGCTTGAGGCGCACTTCCGAGAGAC 1200
DB 1553 GTGCTGTGAGTGTCCCTCTTCTTCTGAGTACAGCTTGAGGCGCACTTCCGAGAGAC 1612
QY 1201 TGCAAGGTGCGCCAGTGGCTCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1260
DB 1613 TGCAAGGTGCGCCAGTGGCTCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1672
QY 1261 CTGAACCTGTATCTACACCATTTGACAGAGAGTCCGCGGTGCTTCCGAGAGATC 1320
DB 1673 CTGAACCTGTATCTACACCATTTGACAGAGAGTCCGCGGTGCTTCCGAGAGATC 1732
QY 1321 CTGAGCGCGCGTGAACCCAGACGAGCTGTGA 1353
DB 1733 CTGAGCGCGCGTGAACCCAGACGAGCTGTGA 1765

RESULT 2
US-09-016-434-1180
Sequence 1180, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1180:
SEQUENCE CHARACTERISTICS:
LENGTH: 3604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9178195
US-09-016-434-1180

Query Match 3.3%; Score 45; DB 4; Length 3604;
Best Local Similarity 100.0%; Pred. No. 6.3e-11;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TCGTCATCGTGACCTGTGCGCATCAGCTGAGACCGCTACTGG 336
DB 2432 TCGTCATCGTGACCTGTGCGCATCAGCTGAGACCGCTACTGG 2476

RESULT 3
US-09-016-434-1256
Sequence 1256, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1256:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1382 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9219405
 US-09-016-434-1256

Query Match 2.9%; Score 39; DB 4; Length 1382;
 Best Local Similarity 100.0%; Pred. No. 3.2e-08;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1141 GTGCTCTGCTGTTCCCTTCTTCTTCAAGCTACAGCCTG 1179
 |||||
 Db 1164 GTGCTCTGCTGTTCCCTTCTTCTTCAAGCTACAGCCTG 1202

Search completed: February 8, 2004, 06:38:57
 Job time : 90.297 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2004, 01:25:52 ; Search time 3134.43 Seconds
(without alignments)
10491.225 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353

Sequence: 1 atggaccacagcagaccctca.....ggaccacagcgcctcgtcga 1353

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 30

Total number of hits satisfying chosen parameters: 193

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 384 | 28.4 | 1044 | 13 | BQ880026 |
| 2 | 47 | 3.5 | 551 | 9 | A1169366 |
| 3 | 47 | 3.5 | 731 | 14 | CAS11027 |
| 4 | 45 | 3.3 | 2410 | 11 | BC035047 |

| | | | | | | |
|----|----|-----|------|----|-----------|--------------------|
| 5 | 44 | 3.3 | 893 | 12 | B1459381 | B1459381 603200147 |
| 6 | 41 | 3.0 | 872 | 29 | ECAA2BAR | AL606560 Horse alp |
| 7 | 39 | 2.9 | 301 | 14 | T39448 | T39448 ya06a09.r2 |
| 8 | 39 | 2.9 | 978 | 13 | BUS39106 | BUS39106 AGENCOURT |
| 9 | 39 | 2.9 | 1031 | 13 | BUS38114 | BUS38114 AGENCOURT |
| 10 | 39 | 2.9 | 1176 | 9 | AL549866 | AL549866 AL549866 |
| 11 | 39 | 2.9 | 1201 | 9 | AL573897 | AL573897 AL573897 |
| 12 | 38 | 2.8 | 988 | 13 | BQ887729 | BQ887729 AGENCOURT |
| 13 | 36 | 2.7 | 256 | 14 | CA315228 | CA315228 UI-M-FW0 |
| 14 | 36 | 2.7 | 1000 | 12 | BG915999 | BG915999 602815267 |
| 15 | 35 | 2.6 | 578 | 14 | CA752540 | CA752540 UI-M-FO0 |
| 16 | 35 | 2.6 | 716 | 28 | AZ286027 | AZ286027 RPCT-23-1 |
| 17 | 35 | 2.6 | 826 | 29 | BZ227940 | BZ227940 CH230-400 |
| 18 | 34 | 2.5 | 683 | 12 | BG830756 | BG830756 602767450 |
| 19 | 34 | 2.5 | 855 | 29 | CGAA23AR | AL606540 Chicken a |
| 20 | 34 | 2.5 | 960 | 13 | BUS38113 | BUS38113 AGENCOURT |
| 21 | 34 | 2.5 | 967 | 29 | CNS03THX | AL259854 Tetradon |
| 22 | 33 | 2.4 | 253 | 28 | AZ632452 | AZ632452 IM0487P03 |
| 23 | 33 | 2.4 | 271 | 10 | BE762670 | BE762670 RC3-NT001 |
| 24 | 33 | 2.4 | 290 | 14 | CD553892 | CD553892 B0367B12- |
| 25 | 33 | 2.4 | 295 | 28 | AZ497396 | AZ497396 IM0334B18 |
| 26 | 33 | 2.4 | 348 | 28 | AO638574 | AO638574 927P1-12C |
| 27 | 33 | 2.4 | 385 | 28 | BH041461 | BH041461 RPCT-24-3 |
| 28 | 33 | 2.4 | 416 | 10 | BB677036 | BB677036 BB677036 |
| 29 | 33 | 2.4 | 418 | 29 | BZ248154 | BZ248154 CH230-498 |
| 30 | 33 | 2.4 | 426 | 29 | BZ232448 | BZ232448 CH230-427 |
| 31 | 33 | 2.4 | 430 | 28 | AZ223727 | AZ223727 RPCT-23-6 |
| 32 | 33 | 2.4 | 451 | 9 | AT461341 | AT461341 fb43d01.x |
| 33 | 33 | 2.4 | 483 | 14 | BT710352 | BT710352 BT710352 |
| 34 | 33 | 2.4 | 485 | 14 | CD553443 | CD553443 B0359G11- |
| 35 | 33 | 2.4 | 568 | 29 | TA161D03P | AL472299 T. brucei |
| 36 | 33 | 2.4 | 573 | 12 | BQ037704 | BQ037704 Pgm1c.DKO |
| 37 | 33 | 2.4 | 600 | 28 | AZ653623 | AZ653623 IM0527E24 |
| 38 | 33 | 2.4 | 672 | 10 | BR625231 | BR625231 BR625231 |
| 39 | 33 | 2.4 | 713 | 28 | AZ288043 | AZ288043 RPCT-23-1 |
| 40 | 33 | 2.4 | 860 | 29 | CNS03HKQ | AL244403 Tetradon |
| 41 | 33 | 2.4 | 887 | 12 | BT734330 | BT734330 60351261 |
| 42 | 33 | 2.4 | 1101 | 29 | CNS052LD | AL118298 Tetradon |
| 43 | 33 | 2.4 | 2758 | 11 | AK004657 | AK004657 Mus muscu |
| 44 | 32 | 2.4 | 167 | 28 | BH072396 | BH072396 RPCT-24-2 |
| 45 | 32 | 2.4 | 350 | 10 | BE648878 | BE648878 UI-M-BH2. |

ALIGNMENTS

RESULT 1
BQ880026
LOCUS
DEFINITION
AGENCOURT 8113358 lupski dorsal root ganglion Homo sapiens cDNA
clone IMAGE:6179035 5', mRNA sequence.
BQ880026
VERSION
BQ880026.1 GI:22272034
ACCESSION
BQ880026
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1044)
NHI-MGC http://mgc.nci.nih.gov/
CDNA Library Prepared by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
plate: LHAM13559 row: 1 column: 20
High quality sequence stop: 430.

FEATURES
source

Seq primer: M13 REVERSE.
Location/Qualifiers

1. 731

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-FJ0-cpv-h-10-0-UI"

/issue_type="embryo"

/dev_stage="embryo"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_1ib="UI-R-FJ0"

/note="Vector: pX-Asc; Site 1: EcoR I; Site 2: Not I; UI-R-FJ0 is a cDNA library containing the following tissue(s): rat embryo. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

BASE COUNT 128 a 217 c 163 g 223 t

Query Match 3.5%; Score 47; DB 14; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.7e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1213 CATGCGCTCTTCAGTCTTCTTCGATCGCTACTGCAACGCTC 1259
42 CATGCGCTCTTCAGTCTTCTTCGATCGCTACTGCAACGCTC 88

RESULT 4 BC035047 2410 bp mRNA 1linear HTC 23-SEP-2002
LOCUS Homo sapiens, Similar to adrenergic, alpha-2A-, receptor, clone
DEFINITION IMAGE:5266354, mRNA.
ACCESSION BC035047.1 GI:23272892
VERSION BC035047.1
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2410)
Strausberg, R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: cgaabs-r@mail.nih.gov
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshitaki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
Contact: amadan@systemsbiology.org
Anup Madan, Jeessica Fahey, Erin Helton, Mark Kerteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRAX Plate: 73 Row: 0 Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15718669
This clone has the following problem: frame shifted.

FEATURES
source

1. 2410

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5266354"

/issue_type="testis"

/clone_1ib="NIH_MGC_97"

/lab_host="DH10B"

/note="Vector: pBluescript"

BASE COUNT 406 a 813 c 721 g 470 t

Query Match 3.3%; Score 45; DB 11; Length 2410;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TCGTCATGTCGACCTGCGCCATGACGCTGACCGCTACTGG 336
Db 568 TCGTCATGTCGACCTGCGCCATGACGCTGACCGCTACTGG 612

RESULT 5 B1459381 893 bp mRNA 1linear EST 21-AUG-2001
LOCUS B1459381 603200147P1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266354 5', mRNA sequence.
DEFINITION B1459381
ACCESSION B1459381 GI:15250037
VERSION B1459381.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 893)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshitaki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: L1AM1671 row: m column: 11
High quality sequence stop: 716.
Location/Qualifiers

FEATURES
source

1. 893

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5266354"

/lab_host="DH10B"

/clone_1ib="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gcgcag); Oligo-dT primed using primer 5'-TTTTTTTTTTT-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT 149 a 303 c 290 g 151 t

ORIGIN

Query Match 3.3%; Score 44; DB 12; Length 893;
 Best Local Similarity 100.0%; Pred. No. 4.3e-09;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 CGTCATCGTGCACCTGTGGCGCATCAGCGCTGACTACTGG 336
 574 CGTCATCGTGCACCTGTGGCGCATCAGCGCTGACTACTGG 617

RESULT 6
 LOCUS ECMA2BAR 872 bp DNA linear GSS 14-SEP-2001
 DEFINITION Horse alpha2 adrenergic receptor gene fragment probably subtype b,
 genomic survey sequence.
 ACCESSION AL606560
 VERSION AL606560.1 GI:15591917
 KEYWORDS GSS; Alpha2 adrenergic receptor gene.
 SOURCE Equus caballus (horse)
 ORGANISM Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 REFERENCE 1 (bases 1 to 872)
 AUTHORS Hunter, C. and Elgar, G.
 TITLE Alpha2 adrenergic receptor gene
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 872)
 AUTHORS Hunter, C.
 TITLE Direct Submission
 JOURNAL Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
 Centre Hinxton, Cambridge, CB10 1SB. UK Email:
 biohel@hgmpr.mrc.ac.uk
 Location/Qualifiers
 source 1..872
 /organism="Equus caballus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9796"

BASE COUNT 156 a 277 c 280 g 159 t

ORIGIN

Query Match 3.0%; Score 41; DB 29; Length 872;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 553 TGCCATCATCATGATCTGTCTACCTGCGCATCTACTGAT 593
 244 TGCCATCATCATGATCTGTCTACCTGCGCATCTACTGAT 284

RESULT 7
 LOCUS T39448 301 bp mRNA linear EST 27-JAN-1995
 DEFINITION y006a09.22 Stragene placenta (#937225) Homo sapiens cDNA clone
 IMAGE:60664 5' similar to similar to SP:A2AD_HUMAN P35369
 ALPBA-2C-2 ADRENERGIC mRNA sequence.
 ACCESSION T39448.1 GI:647179
 VERSION T39448.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 301)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gib, M., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Maridis, E., Moore
 Schellenberg, K., Soares, M.B., Tan, F., Thierly-Weg, J., Trevaaks, E.,
 Underberg, K., Woldmann, P., Watsen, R., Wilson, R. and Marra, M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 PUBMED 8889549

COMMENT Other ESTs: y006a09.a1
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: M13RP1.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:60664"
 /sex="male"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene placenta (#937225)"
 /note="Organ: placenta; Vector: pBluescript SK-; Site 1:
 EcorI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
 XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
 adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

BASE COUNT 40 a 107 c 71 g 83 t

ORIGIN

Query Match 2.9%; Score 39; DB 14; Length 301;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1141 GTGCTTCGCTGCTCCCTCTTCTTCTGAGCTACAGCCTG 1179
 114 GTGCTTCGCTGCTCCCTCTTCTTCTGAGCTACAGCCTG 152

RESULT 8
 LOCUS BUS39106 978 bp mRNA linear EST 13-SEP-2002
 DEFINITION AGNCOURT_10215036 NIH_MGC_107 Homo sapiens cDNA clone
 IMAGE:6569764 5', mRNA sequence.
 ACCESSION BUS39106
 VERSION BUS39106.1 GI:22849547
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 978)
 AUTHORS NIH-MGC http://imgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rt@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LNC2757 row: j column: 04
 High quality sequence stop: 554.
 Location/Qualifiers
 source 1..978
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6569764"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_107"

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BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. Contact : Peng Liang Email: liang@lfeech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope Sequence ID : CS01054DD01N1.

FEATURES

Source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1054YH02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_1b="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      193 a      391 c      364 g      205 t      48 others
ORIGIN

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Query Match 2.9%; Score 39; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred.No. 9e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|------|-------------------------------------|------|
| QY | 1141 | GTGCTCTGCTGGTTCCTTCTTTCAGCTACAGCTTG | 1179 |
| | | | |
| Db | 733 | GTGCTCTGCTGGTTCCTTCTTTCAGCTACAGCTTG | 695 |
| | | | |

RESULT 12

| | | | | | |
|------------|--------------------|-------------|--------------|------------|-----------------|
| LOCUS | BQ887729 | 988 bp | mRNA | linear | EST 16-AUG-2002 |
| DEFINITION | AGENCOURT_8764335 | NIH_MGC_129 | Mus musculus | cdna clone | IMAGE:63131333 |
| | 5', mRNA sequence. | | | | |

| | |
|-----------|---------------------|
| ACCESSION | BQ887729 |
| VERSION | BQ887729.1 |
| KEYWORDS | GI:22279743 EST. |

REFERENCE 1 (bases 1 to 988)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

| Query Match | 2.8%; | Score 38; | DB 13; | Length 988; |
|-------------|-------|-----------|--------|-------------|
|-------------|-------|-----------|--------|-------------|

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Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 274 GACGTGCTCTTGACACCTCGTCCATCGTGACCTGTG 311
|||
Db 188 GACGTGCTCTTGACACCTCGTCCATCGTGACACCTGTG 225

RESULT 1.3

| | | | | | |
|------------|---|--------|------|--------|-----------------|
| LOCUS | CA315228 | 256 bp | mRNA | linear | EST 26-NOV-2002 |
| DEFINITION | UT-M-FW0-cbi-b-15-0-UT.r1 NIH BMP_FW0 Mus musculus cDNA clone | | | | |
| IMAGE | IMAGE: 6809872.5', mRNA sequence. | | | | |
| ACCESSION | CA315228 | | | | |

| | | |
|-----------|----------------------------|-------------|
| ACCESSION | CA315228 | GI:24533352 |
| VERSION | CA315228.1 | |
| KEYWORDS | EST. | |
| SOURCE | Mus musculus (house mouse) | |
| ORGANISM | Mus musculus | |

| | |
|-----------|---|
| REFERENCE | 1 (bases 1 to 256) |
| AUTHORS | NIH-MGC http://mgc.mci.nih.gov/ . |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) |
| JOURNAL | Unpublished |
| COMMENT | Contact: Robert Strausberg, Ph.D. |

The following repetitive elements were found in this cDNA sequence: 37-156, >(GGA)nSimple repeat (matched complement) 82-200, >(GAA)nSimple repeat (matched complement) 201-254, >(GCA)nSimple repeat (matched complement)
Seq primer: pYX-5.

FEATURES

Source

| BASE COUNT | 7 a | 140 c | 9 g | 100 t |
|------------|-----|-------|-----|-------|
| ORIGIN | | | | |

| | | | | |
|--------------------------|--------|--------------------|-----------|-------------|
| Query Match | 2.7% | Score 36; | DB 14; | Length 256; |
| Best Local Similarity | 100.0% | Pred. NO. 1.6e-05; | | |
| Matches 36; Conservative | 0; | Mismatches 0; | Indels 0; | Gaps 0 |

QY 892 GAAGAGAGAGAGAGAGAGAGAGAGAGAG 927
 ||||||||||||||||||||||||||||||||||
 DB 89 GAAGAGAGAGAGAGAGAGAGAGAGAGAG 54

RESULT 14
 BG915999 1000 bp mRNA linear EST 05-JUN-2001
 LOCUS 602815267F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4937465 5',
 DEFINITION mRNA sequence.
 ACCESSION BG915999
 VERSION BG915999.1 GI:14296475
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1000)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
 Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10871 row: e column: 18
 High quality sequence stop: 486.

FEATURES
 source Location/Qualifiers
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 /mol_type="mRNA"
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 /clone="IMAGE:4937465"
 /cissue_type="tumor, gross tissue"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Mam4"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Priscilla Furth,
 NIH Reference for transgenic model: Li et al., Cell Growth
 and Differentiation 7, 3-11 (1996)."

BASE COUNT 358 a 202 c 240 g 200 t

ORIGIN

Query Match 2.7%; Score 36; DB 12; Length 1000;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 892 GAAGAGAGAGAGAGAGAGAGAGAGAGAG 927
 ||||||||||||||||||||||||||||||||||
 DB 37 GAAGAGAGAGAGAGAGAGAGAGAGAGAG 72

RESULT 15
 CA752540 578 bp mRNA linear EST 27-NOV-2002
 LOCUS UI-M-FOO-cdo-g-14-0-UI.r1 NIH_BMAP_FOO Mus musculus cDNA clone
 DEFINITION IMAGE: 6831111 5', mRNA sequence.
 ACCESSION CA752540
 VERSION CA752540.1 GI:25583363
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 1 (bases 1 to 578)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 The following repetitive elements were found in this cDNA
 sequence: 24-142, >(GGA)n#Simple_repeat (matched complement)
 158-277, >(GGA)n#Simple_repeat (matched complement) 301-578,
 >RMR17C#LTR_5/6_bp_duplication
 Seq primer: pyx-5

FEATURES
 source Location/Qualifiers
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 /mol_type="mRNA"
 /strain="C57BL/6"
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 /clone="IMAGE: 6831111"
 /cissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP F00"
 /note="Organ: Brain; Vector: pyx-Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is TGAGAGAGCC. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

BASE COUNT 33 a 289 c 24 g 232 t

ORIGIN

Query Match 2.6%; Score 35; DB 14; Length 578;
 Best Local Similarity 100.0%; Pred. No. 5.5e-05;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 892 GAAGAGAGAGAGAGAGAGAGAGAGAGAG 926
 ||||||||||||||||||||||||||||||||||
 DB 386 GAAGAGAGAGAGAGAGAGAGAGAGAGAG 352

Search completed: February 8, 2004, 06:35:51
 Job time : 3142.43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:44:02 ; Search time 519.53 Seconds
(without alignments)
10811.687 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353
Sequence: 1 atgagaccacagaccaccta.....ggaccacagcgccgcgtga 1353

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sca:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sca:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pin:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|---------------------|
| 1 | 1353 | 100.0 | 1353 | 6 AX350489 | AX350489 Sequence |
| 2 | 1353 | 100.0 | 9842 | 6 AF005900 | AF005900 Homo sapi |
| 3 | 1349.8 | 99.8 | 2072 | 6 AR270618 | AR270618 Sequence |
| 4 | 1349.8 | 99.8 | 2072 | 6 HUMADRA2RA | M34041 Human alpha |
| 5 | 1349.8 | 99.8 | 3274 | 6 AX548756 | AX548756 Sequence |
| 6 | 1325 | 97.9 | 1344 | 6 AX350490 | AX350490 Sequence |
| 7 | 1325 | 97.9 | 1344 | 6 AF316895 | AF316895 Homo sapi |
| 8 | 1321.8 | 97.7 | 22842 | 9 AC092603 | AC092603 Homo sapi |
| 9 | 1159.2 | 85.7 | 1356 | 4 AY150333 | AY150333 Tupiaia de |
| 10 | 1046 | 77.3 | 1987 | 10 CP025723 | U25723 Cavia porce |
| 11 | 989.2 | 73.1 | 1639 | 10 RNA2BRRA | X74400 R.norvegicu |
| 12 | 988.8 | 73.1 | 6268 | 10 AF366899 | AF366899 Rattus no |
| 13 | 988.8 | 73.1 | 124474 | 2 AC126878 | AC126878 Rattus no |
| 14 | 984 | 72.7 | 22319 | 10 RAT2BR | M32061 Rat alpha-2 |
| 15 | 977.8 | 72.3 | 276543 | 2 AC112830 | AC112830 Rattus no |
| 16 | 977.6 | 72.3 | 1347 | 10 AF332049 | AF332049 Mus muscu |
| 17 | 977.6 | 72.1 | 1650 | 10 MUSADRENH | L00979 Mus musculu |
| 18 | 976 | 72.1 | 1347 | 10 AF332050 | AF332050 Mus muscu |
| 19 | 976 | 72.1 | 83802 | 10 AL731836 | AL731836 Mouse DNA |
| 20 | 975.2 | 72.1 | 1185 | 10 ASP427259 | AJ427259 Anomaluru |
| 21 | 968 | 71.5 | 1185 | 10 EDO427270 | AJ427270 Eretichon |
| 22 | 967.4 | 71.5 | 1180 | 9 NC0251186 | AJ251186 Nycticebu |
| 23 | 965.4 | 71.3 | 1171 | 9 CVA251182 | AJ251182 Cynoceph |
| 24 | 964.6 | 71.3 | 1203 | 4 TTE315939 | AJ315939 Tapirus t |
| 25 | 962.6 | 71.1 | 1191 | 10 CCA437260 | AJ427260 Castor ca |
| 26 | 961 | 71.0 | 1168 | 4 TTR251187 | AJ251187 Tupiaia ta |
| 27 | 960.6 | 71.0 | 1197 | 4 LCR427254 | AJ427254 Lepus cra |
| 28 | 960 | 71.0 | 9377 | 10 MUSADRECA | M94583 Mus musculu |
| 29 | 957.4 | 70.8 | 1183 | 4 OCAR2B | Y15946 Oryctolagus |
| 30 | 954.6 | 70.6 | 1197 | 4 LPA315941 | AJ315941 Lama paco |
| 31 | 951.8 | 70.3 | 1185 | 10 GGL427258 | AJ427258 Gila glis |
| 32 | 950 | 70.2 | 1198 | 4 ECAR2B | Y15945 Equus cabal |
| 33 | 949.4 | 70.2 | 1183 | 4 OCY16189 | Y16189 Oryctolagus |
| 34 | 948.8 | 70.1 | 1180 | 4 LPA505821 | AJ505821 Lama paco |
| 35 | 945.4 | 69.9 | 1177 | 4 BPH251175 | AJ251175 Balaeopt |
| 36 | 939.8 | 69.5 | 1180 | 4 HAM251178 | AJ251178 Hippopota |
| 37 | 938.4 | 69.4 | 1186 | 4 MSP251185 | AJ251185 Manis sp. |
| 38 | 938.2 | 69.3 | 1172 | 10 ARU427256 | AJ427256 Apidontci |
| 39 | 937.6 | 69.3 | 1179 | 10 TPA427266 | AJ427266 Trichys f |
| 40 | 936.2 | 69.2 | 1197 | 4 MTE505820 | AJ505820 Manis tat |
| 41 | 932.4 | 68.9 | 1162 | 4 FCA251174 | AJ251174 Felis cat |
| 42 | 932.2 | 68.9 | 1185 | 4 AF337541 | AF337541 Tonatia b |
| 43 | 931.4 | 68.8 | 1174 | 4 PCA427417 | AJ427417 Physter |
| 44 | 931.2 | 68.8 | 1168 | 4 PVI251176 | AJ251176 Phoca vit |
| 45 | 930 | 68.7 | 1176 | 4 LAL315940 | AJ315940 Lagenorhy |

ALIGNMENTS

RESULT 1
AX350489
LOCUS AX350489 1353 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 1 25-OCT-2001;

Prod. No. is the number of results predicted by chance to have a

Db 593 GTGGCCACGCTCATCTCCCTTTCTGTGGCCACAGAGCTGTGGGCTTACTGTCTTC 652
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 Db 653 CGGGGCACTGTGGGAGGTGTACTGTGGGCTTGAAGTGTCTTTGTGACCTTGTGTCATC 712
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 Db 713 GTGGCACTGTGGGCACTGTGACCGGTACTGTGGGCGGTGAGCGGGGCTGAGTAC 772
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 Db 773 AACTCCAAAGGCGACCCCGGCGGCACTGAAGTGCATATCTTCACTGTGTGCTCATGCGC 832
 QY 421 GCGGTCACTGTGGGCGGCTCATCTCAAGAGGCGGTGACCTGTGGGCGGTGAGTAC 480
 Db 833 GCGGTCACTGTGGGCGGCTCATCTCAAGAGGCGGTGACCTGTGGGCGGTGAGTAC 892
 QY 481 GCGGTCACTGTGGGCGGCTCATCTCAAGAGGCGGTGACCTGTGGGCGGTGAGTAC 952
 Db 893 GCGGTCACTGTGGGCGGCTCATCTCAAGAGGCGGTGACCTGTGGGCGGTGAGTAC 952
 QY 541 TTCTTTGCTCTGTGGCTCATCTCAAGAGGCGGTGACCTGTGGGCGGTGAGTAC 600
 Db 953 TTCTTTGCTCTGTGGCTCATCTCAAGAGGCGGTGACCTGTGGGCGGTGAGTAC 1012
 QY 601 CGGACGACCGGACAGTGTCCAGAGGCGGCGGCTGTGGGCGGCGGTGAGTAC 660
 Db 1013 CGGACGACCGGACAGTGTCCAGAGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1072
 QY 661 CGGACGACCGGACAGTGTCCAGAGGCGGCGGCTGTGGGCGGCGGTGAGTAC 720
 Db 1073 CGGACGACCGGACAGTGTCCAGAGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1132
 QY 721 GCTTGTGCAAGAGTGTCAAGAGGCGGCGGCTGTGGGCGGCGGTGAGTAC 780
 Db 1133 GCTTGTGCAAGAGTGTCAAGAGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1192
 QY 781 ACCCTGAAGTGTCTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 840
 Db 1193 ACCCTGAAGTGTCTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1252
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 Db 1253 GCGGACGCGGACAGAGGAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1312
 QY 901 GAAAGAGAGAGAGAGAGAGAGTGTGAACCCGAGGCGGCGGCTGTGGGCGGCGGTGAGTAC 960
 Db 1313 GAAAGAGAGAGAGAGAGAGAGTGTGAACCCGAGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1372
 QY 961 TCAAGCTTGCAGGCGGCGGCTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1020
 Db 1373 TCAAGCTTGCAGGCGGCGGCTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1432
 QY 1021 GCGGACGCGGACAGAGGAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1080
 Db 1433 GCGGACGCGGACAGAGGAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1492
 QY 1081 GCGGACGCGGACAGAGGAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1140
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 Db 1553 GTGCTGTGCTGTGGTCTTCTTCTTCAAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1612
 QY 1201 TGCAGAGTGTGCTGTGGTCTTCTTCTTCAAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1260
 Db 1613 TGCAGAGTGTGCTGTGGTCTTCTTCTTCAAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1672
 QY 1261 CTGAACCTGTGTATCTTCAAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1320
 Db 1673 CTGAACCTGTGTATCTTCAAGTGTGTGGGCGGCGGCTGTGGGCGGCGGTGAGTAC 1732

QY 1321 CTGTCGCGCGCGGTGAGACCCAGAGCGGCTGTGTA 1353
 Db 1733 CTGTCGCGCGCGGTGAGACCCAGAGCGGCTGTGTA 1765
 RESULT 4
 HUMADRA2RA
 LOCUS
 DEFINITION
 ACCSSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 HUMAN
 Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 2072)
 Yang-Feng, T.L., Caron, M.G. and Leffkowitz, R.J.
 Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
 90311349
 MEDLINE
 JOURNAL
 COMMENT
 Original source text: Human placenta DNA, clone alpha-2 C2. Draft entry and computer-readable sequence for (1) kindly submitted by J.W.Lomasney, 03-MAY-1990, for release after publication.
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 BASE COUNT
 ORIGIN
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 Query Match 99.8%; Score 1349.8; DB 9; Length 2072;
 Best Local Similarity 99.8%; Pred. No. 2.9e-217;
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 QY 61 TTCTTCATTTCTTTTACATCTTGGGCAAGCTCTGTGTCATCTGTGTGTTGACGAGC 120
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| OY | 181 | GTGGCGCAGCTCATATATCCCTTTCGCTGGCGCAACGAGCTGCTGGGCTACCTGGATCTC | 240 |
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| OY | 241 | CGGCGCAGTGGGTGCGAGTGTACTTGGCGGCTCGACGTGCTCTTCTGCACTCTGTCAATC | 300 |
| Db | 653 | CGGCGCAGTGGGTGCGAGTGTACTTGGCGGCTCGACGTGCTCTTCTGCACTCTGTCAATC | 712 |
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| Db | 713 | GTGCACTGTGGCCATCAGCCTGGAGCCGCTACCTGGGCCGTGGAGCCGCGCCTGGAGTAC | 772 |
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| Db | 833 | GCCTGCATCTGCTGCTCGCGCCCTCATCTTACAAAGGGCGACCAAGGGCCCCCAGCGCGGG | 892 |
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| Db | 953 | TTCTTTGCTCTTGTGCTCATCATGATCTCTTGTCTTACTCTGGCATTTACTGATGCCAA | 1012 |
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| Db | 1013 | CGCAGCAACCCGAGAGTCCAGGGGCCAAAGGGGGGCTTGGCGAGGGTGAATCCAAAGAG | 1072 |
| OY | 661 | CCCCGACCCGACCAATGTGTGGGCTTTGGGCTCAGCGCAAACTGGCCAGCCCTGAGCTCTGTG | 720 |
| Db | 1073 | CCCCGACCCGACCAATGTGTGGGCTTTGGGCTCAGCGCAAACTGGCCAGCCCTGAGCTCTGTG | 1132 |
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| OY | 1021 | GGCCAGGTGCTCTGGGAGAGGGGCGTGGGTCTAATAGTGGGCAAGTGTGGCGTTCGAAG | 1080 |
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| OY | 1141 | GTGCTCTGCTGATCCCTTCTTCTTCAAGCTAACAGCTTGGGCGCCATCTGCCGGAAGAC | 1200 |
| Db | 1553 | GTGCTCTGCTGATCCCTTCTTCTTCAAGCTAACAGCTTGGGCGCCATCTGCCGGAAGAC | 1612 |
| OY | 1201 | TGCAGAGTGGCCCAATGAGCTCTTCCAGTTCTTCTTGTGAATCGGCTAATCGCAACGCTCA | 1260 |
| Db | 1613 | TGCAGAGTGGCCCAATGAGCTCTTCCAGTTCTTCTTGTGAATCGGCTAATCGCAACGCTCA | 1672 |

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| LOCUS | AX548756 | | | | |
| DEFINITION | Sequence 41 from Patent WO02061087. | | | | |
| ACCESSION | AX548756 | | | | |
| VERSION | AX548756.1 | GI:25813686 | | | |
| KEYWORDS | | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| AUTHORS | 1 | | | | |
| TITLE | Burner,G.C., Roush,C.T., and Brown,J.P. Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides Patent: WO 02061087-A 41 08-AUG-2002; Lifespan Biosciences, Inc. (US) Location/Qualifiers 1..3274 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" | | | | |
| JOURNAL | | | | | |
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| BASE COUNT | 587 a 979 c 967 g 741 t | | | | |
| ORIGIN | | | | | |
| Query Match | 99.8%; Score 1349.8; DB 6; Length 3274; | | | | |
| Best Local Similarity | 99.9%; Pred. No. 2.8e-217; | | | | |
| Matches 1351; Conservative | 0; Mismatches 2; Indels 0; Gaps 0; | | | | |
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| Db | 1 ATGAGACCAACGAGACCCCTACTCCGTGACGAGCCACAGCGGCGCATAGCGGCGGCATACAC | 60 | | | |
| OY | 61 TTCCTCATCTCTTACCATCTTTCGGGACGCTCTGATCATCTGGCTGTGTGACGAGC | 120 | | | |
| Db | 61 TTCCTCATCTCTTACCATCTTTCGGGACGCTCTGATCATCTGGCTGTGTGACGAGC | 120 | | | |
| OY | 121 CGCTCGCTGCGCGCCCTCAGAACTGTTCTGTGTGCTGCTGGCCGCCCGGACATCTCTG | 180 | | | |
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| OY | 481 CGCCCTCAATGCAAGCTTCAACAGAGGCGCTGTATCTGTGGCTTCAGCATGGAATCT | 540 | | | |
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LOCUS Sequence 2 from Patent WO0179561.
ACCESSION AX350490
VERSION AX350490.1 GI:18616092
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms

JOURNAL Patent: WO 0179561-A 2 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
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QY 781 ACCCTGAAGATACGTGGAGCCCGGAGCTTTCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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[illegible]

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| REFERENCE | 4 (bases 1 to 22842) |
| AUTHORS | Waterston,R.H. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA |
| REFERENCE | 5 (bases 1 to 22842) |
| AUTHORS | Waterston,R.H. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA |
| REFERENCE | 6 (bases 1 to 22842) |
| AUTHORS | Waterston,R. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA |
| COMMENT | On Oct 20, 2001 this sequence version replaced gi:14916188. |

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone, and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RPci-11 human BAC library was made from the blood of one male donor, as described by Oogawara, K., Woon, P.-Y., Zhao, B., Frengen, E., Tatematsu, M., Cacanese, J.J., and de Jong, P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.regen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-401C13, 2000 bp overlap; the clone sequenced to the right is RP11-574O17, 2000 bp overlap. Actual end of this clone is at base position 48999 of RP11-574O17.

Polymorphisms have been identified between AC013272 and AC092603.

The sequence of AC073396 has been incorporated into AC092603.

FEATURES

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| Best Local Similarity | 99.2%; Pred. No.1.le-212; | |
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| Db | 15030 | GTGCACCTGTGCGGCATCAGCTTGAGCCGCTACTGAGCCGTGAGCCGCGCTGAGATAC 14971 |
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| Db | 14970 | AACCTCAAGGCAACCCCGCGCCGCATCAAGTGTATATCTCACTGTGTGCTCATCGCC 14911 |
| QY | 421 | GCGCTCATCTCGCTGCGCCCTCATCTCAAGGAGCAACAGGACCCCGACGCGCGGG 480 |
| Db | 14910 | GCGCTCATCTCGCTGCGCCCTCATCTCAAGGAGCAACAGGACCCCGACGCGCGGG 14851 |
| QY | 481 | CGCCCCAGTGCAGAGCTCAACAGAGGCGTGTATCATCTTGACCTCAAGATCGGATCT 540 |
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| QY | 541 | TTCTTTGCTCTCTTGCCCTCATCATGATCTTGTCTACTCTGCGCATCTACTGATCGCAAA 600 |
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| Db | 14730 | CGCAGCAACCGCAGAGGTCCAGAGGCGCAAGGGGGGGCGCTGGCGAGGGGTGATCTCAAGCAG 14671 |
| QY | 661 | CCCCGACCGACATGGTGGGGGCTTTGGCTCAGCCAACTGCGCAAGCCCTGGGCTTCTGTG 720 |

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Db 14550 ACCCTTGAAATATCTGGGACCCGGGCTTGGCCAGTCAGTTGGGCTGCCCTTCCAACTCA 14491
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RESULT 9
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LOCUS Tupaiia belangeri alpha-2B adrenoceptor mRNA, complete cds.
DEFINITION
AY150333
VERSION
AY150333.1 GI:25298985
KEYWORDS
SOURCE
ORGANISM
Tupaiia belangeri (tree shrew)
Tupaiia belangeri
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
REFERENCE
1 (bases 1 to 1356)
Helbronner, U., van Kampen, M., Isovich, E. and Fluegge, G.
Thalamic alpha-2B adrenoceptors under chronic stress: persistent
upregulation in the paraventricular nucleus
unpublished
2 (bases 1 to 1356)
Fluegge, G. and Meyer, H.
Direct Submission
Submitted (13-SEP-2002) Neurobiology, German Primate Center (DPZ),
Kellnerweg 4, Goettingen 37077, Germany
LOCATION/Qualifiers
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Qy      838 TGAAGCCAGGCGCCAGAGAGGGTGTGTTGTGGGCGATCTTCAGAGAGTAAGCTGAAG 897
Db      841 TCAGGCGCAGGGCCAGAGAGGGGTGTGTTGTGGGCGATCTTCAGAGAGTAAGAG 900
Qy      898 GAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
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LOCUS      CPU25723
DEFINITION      Cavia porcellus alpha-2B adrenoceptor gene, complete cds.
ACCESSION      U25723
VERSION      U25723.1 GI:818876
KEYWORDS
SOURCE
ORGANISM      Cavia porcellus (domestic guinea pig)
Cavia porcellus
Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystriognathia; Cavidae; Cavia.
REFERENCE
AUTHORS      Svensson,S.P., Bailey,T.J., Porter,A.C., Richman,J.G. and
              Regan,J.W.
TITLE      Heterologous expression of the cloned guinea pig alpha 2A, alpha
              2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and
              functional coupling to a CAMP-responsive reporter gene
JOURNAL      Biochem. Pharmacol. 51 (3), 291-300 (1996)
MEDLINE      96152573
PUBMED      8573196
REFERENCE
AUTHORS      Richman,J.G.
TITLE      Direct Substitution
JOURNAL      Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
              Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
              AZ 85721, USA
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 ACCESSION X74400.1 GI:840862
 VERSION alpha-2B-adrenergic receptor; epinephrine-binding; G-protein
 KEYWORDS coupled receptor; norepinephrine-binding; transmembrane receptor.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 Le Jossac M., Cloix J.F., Pecquery R., Giudicelli Y. and
 AUTHORS Dausse J.P.
 TITLE Differential sodium regulation between salt-sensitive and
 salt-resistant Sabra rats is not due to any mutation in the renal
 alpha 2B-adrenoceptor gene
 JOURNAL Am. J. Hypertens. 8 (2), 177-182 (1995)
 MEDLINE 95275492
 PUBMED 7755946
 REFERENCE 2 (bases 1 to 1639)
 AUTHORS Le Jossac M.M.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUL-1993) M.M. Le Jossac, Groupe de Signalisation,
 Service de Biochimie, Paris-Ouest, 45 rue des Saintes Peres, 75270
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 REMARK sequence revised by author 09-SEP-1993
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| Db | 898 CTATCTTTCTGTTGGAGAGGCCAATGGAACCCCAAGCCTCCAAAGAGAGAGAGAGAGGG 957 |
| Qy | 778 GAGACCCCTGAAGATCTGGGACCCGGGCGTTGGCCACGATGGGCGTCCCTTCCCAAC 837 |
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| Qy | 1318 ATCTGTGCGCGCGGTGAGACCCAGCGGCTGTGTA 1353 |
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| LOCUS | |
| DEFINITION | Rattus norvegicus alpha2B-adrenergic receptor (Rng) gene, complete cds. |
| ACCESSION | AF366899 |
| VERSION | AF366899.1 GI:14039788 |
| KEYWORDS | |
| SOURCE | Rattus norvegicus (Norway rat) |
| ORGANISM | Rattus norvegicus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |
| AUTHORS | 1 (bases 1 to 6268) |
| TITLE | Schaak,S., Cussac,D. and Parle,H. |
| JOURNAL | Cloning and characterization of the rat alpha2B-adrenergic receptor gene promoter |
| REFERENCE | Unpublished |
| AUTHORS | 2 (bases 1 to 6268) |
| TITLE | Schaak,S., Cussac,D. and Parle,H. |
| JOURNAL | Direct Submission |
| FEATURES | Submitted (29-MAR-2001) U388, INSERM, CHU Rangueil, Toulouse 31403, France |

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| Blast Local Similarity | 84.2%; Pred. No. 1.3e-156; | | |
| Matches 1142; Conservative 0; Mismatches 202; Indels 12; Gaps 2; | | | |
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| Oy | 301 GTGCACCTGTGTGCGCATCAAGCTTGAGACCGCTACTGTGGCCGTGAGCCGCGCGCTGAGATAC 360 | | |
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| Oy | 361 AATCCGAAGGCAACCCCGCGCCGATCAATGTGATCATCTCACTGTGTGGCTCATCGCC 420 | | |
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OY 1018 CGTGGCCAGGCTGCTTCTGCGGCGAGGCGGCTGTATAGTGGGCGAGTGGCTCGA 1077
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RESULT 13
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LOCUS Ratius norvegicus clone CH230-263M16, WORKING DRAFT SEQUENCE, 2
DEFINITION unoriented pieces.
ACCESSION AC126878
VERSION AC126878.4 GI:25007910
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

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SOURCE

Rattus norvegicus (Norway rat)

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 124474)
Muzny, D., Marie, M., Metker, M., Lee, A., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alebrooks, S., Amth, A., Angilano, D.,
Anylebech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryan, N., Bunay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Cester, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Dermo, C., Ding, Y., Dinh, H., Divya, K.,
Diaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Gervais, W.,
Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
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Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshew, L., Louiseged, H., Lozano, R. J., Lu, X., Ma, D.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Muniz, M., Murphy, M., Nait, L.,
Nankervyls, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwokedeme, O., Okunolu, G., Olarnunsgoon, A., Pal, S., Parks, K.,
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Plopper, F., Poindexter, A., Popovic, D., Prims, E., Pu, L.,
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Register, M. A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rivers, C., Rodley, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smaj, D.,
Sneely, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uman, K.,
Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yeon, L., Yeon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.

TITLE

Unpublished

REFERENCE

2 (bases 1 to 124474)
Worley, K. C.

REFERENCE

Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

REFERENCE

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

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Baylor Plaza, Houston, TX 77030, USA

REFERENCE

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

COMMENT

The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Aclas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

| QY | 1138 | TTTATGCTGCTGCTGCTTCCCTTCTTCTTCAAGCTACAGACCTGGAGCGCAATCTGCGGAAG | 1197 |
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| QY | 58635 | TTTCGGGTCTGCTGCTGCTTCTTCTTCTTCAAGCTACAGACCTGGAGCGCAATCTGCGGAAG | 58695 |
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| Db | 58755 | TCTTTGAACCCCTGTATATCTACACAGCGTCTTCAACAGAGATTTCCGCGCGTCTTCGAAGG | 58815 |
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| RESULT | 14 | | | | |
| RAT2BR | RATA2BR | 2319 bp | mRNA | linear | ROD 27-APR-1993 |
| LOCUS | Rat alpha-2B-adrenergic receptor (RNG-alpha-2) | | | | |
| DEFINITION | M32061 | | | | |
| ACCESSION | M32061.1 | GI:202589 | | | |
| VERSION | adrenergic receptor. | | | | |
| KEYWORDS | Rattus norvegicus (Norway rat) | | | | |
| SOURCE | Rattus norvegicus | | | | |
| ORGANISM | Rattus norvegicus | | | | |

| REFERENCE | AUTHORS | TITLE | JOURNAL | MEDLINE | PUBMED | COMMENT |
|---------------------|---|--|--|---------|---------|---|
| 1 (bases 1 to 2319) | Zeng,D.W., Harrison,J.K., D'Angelo,D.D., Barber,C.M., Tucker,A.L., Lu,Z.H. and Lynch,K.R. | Molecular characterization of a rat alpha 2B-adrenergic receptor | Proc. Natl. Acad. Sci. U.S.A. 87 (8), 3102-3106 (1990) | 9023217 | 2158103 | Original source text: Rat (strain Sprague Dawley) adult kidney, |

FEATURES

Draft entry and computer-readable sequence [1] kindly submitted by
K.R.Lynch, 12-FEB-1990.
Location/Qualifiers

| FEATURES | Location/Qualifiers |
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Query Match      72.7%; Score 984; DB 10; Length 2319;
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Matches 1139; Conservative 0; Mismatches 205; Indels 12; Gaps 2;

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| QY | 61 | TTCCCTCATTTCTTTTACCATCTTTCGAGCAAGCTCTGCTCATCTCGCTGTGTGGACAGC | 120 |
| Db | 441 | TTTCTCATCTTTTTCACCATTTTTCGGAATGCGCTGGTCTATTGCTGTGTGGACAGC | 500 |
| QY | 121 | CGCTCGTGCAGCGCCCTCAGAACTGTCTGTGTGTGCTGGCCGCGCCGACATCTCTG | 180 |
| Db | 501 | CGCTCATCGGTGCACCAAAAACCTGTTCTGTGTGTCTACCTGGCAGCAGCCGACATCTTA | 560 |
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| Db | 561 | GTGGCTACTCTCATCATCTCCCTTTCTCTGTGCACCAAGCTGGCTGGGCTACTGGTACTTC | 620 |
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| DEFINITION | AC112830 276543 bp DNA linear HTG 11-SEP-2002 | | |
| ACCESSION | AC112830 | | |
| VERSION | AC112830.3 GI:23266028 | | |
| KEYWORDS | HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED. | | |
| SOURCE | Rattus norvegicus (Norway rat) | | |
| ORGANISM | Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | |
| REFERENCE | 1 (bases 1 to 276543) | | |
| AUTHORS | Muzny,D,Merle, Metzker,M, Lee, Abramzon,S, Adams,C, Alder,J, Allen,C, Allen,H, Albrooke,S, Amin,A, Anguiano,D, Anyalabechei,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H, Baldwin,D, Bandaranaike,D, Barber,M, Bainsstead,M, Benahmed,F, Blawalo,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M, Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E, Cardenas,V, Carter,K, Cavazos,I, Cesaar,H, Center,A, Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J, Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L, Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D, Delgado,O, Denon,S, Deramo,C, Ding,Y, Dinh,H, Divya,K, Diaper,H, Dugan-Rocha,S, Dunn,A, Durdin,K, Duval,B, Eaves,K, Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G, Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P, Freiser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M, Gegeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,W, Gunaratne,P, Haaland,W, Hamli,C, Hamilton,C, Hamilton,K, Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J, Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M, Hollins,B, Howells,S, Huliyk,S, Hume,J, Idlebird,D, Jackson,A, Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A, Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C, Kovis,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J, Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J, Lorenshawea,L, Louiseged,H, Losado,R,J, Lu,X, Ma,J, Maheshwari,M, Mahindaratne,M, Mahmoud,M, Malloy,K, Mangun,A, Mangum,B, Meguru,P, Martin,K, Martin,R, Martinez,E, Mahoney,S, McLeod,M,P, McNell,T,Z, Meenen,E, Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S, Morgan,M, Morris,K, Morris,S, Mungata,M, Murphy,M, Natir,L, Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S, Nwokilehem,O, Okwono,G, Olariuonagoun,A, Pal,S, Parke,K, Paternack,S, Paul,H, Perez,A, Perez,L, Pfankoch,C, Plopper,F, Poindexter,A, Popovic,D, Prims,B, Pu,L-L, Puzo,M, Qulroz,J, Rachin,E, Reeves,K, Regier,M,A, Reigh,R, Kelly,B, Kelly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F, | | |

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Sander, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
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Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smaj, D.,
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Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 276543)
Worley, K. C.
Direct Submission
Submitted (25-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 276543)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (21-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 21, 2002 this sequence version replaced gi:21743329.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GRPO
Center clone name: CH230-46115
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 237012 bases at least Q40
Consensus quality: 239346 bases at least Q30
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Estimated insert size: 252028; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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COMMENT
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BASE COUNT      60488 a 57895 c 60622 g 63094 t 34444 others
ORIGIN

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 Best Local Similarity 84.2%; Pred. No. 5.7e-155;
 Matches 1142; Conservative 0; Mismatches 202; Indels 13; Gaps 3;

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[illegible]

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| Qy | 1021 | GGCCAGGTGCTCTGTGGCAGAGGGGAGTGGGATCTTAAGTGTGGCAGTGGTGGCTTCGAAG | 1080 |
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| Qy | 1141 | GTCGCTGCTGCTTCCCTCTTCTTTCAAGCTACAGCCTGTGGCGGCATCTGCCCCAAGAC | 1200 |
| Dp | 1141 | GTCGCTGCTGCTTCCCTCTTCTTTCAAGCTACAGCCTGTGGCGGCATCTGCCCCAAGAC | 1200 |

| QY | 1201 | TCGAAGTGGCCCCATGAGGCTCTTCCAGTTCTTCTTTGGAATCGGCTACTGGAACAGCTCA | 1260 | | | |
|---|--|--|------|--|--|--|
| DB | 1201 | TGCAGAGGTGCCCCATGAGGCTCTTCCAGTTCTTCTTTGGAATCGGCTACTGGAACAGCTCA | 1260 | | | |
| OY | 1261 | CTGAACCTGTATTACTACACCATCTTCAACGAGACTTCGCGCTGCTTCCGAGGATC | 1320 | | | |
| DB | 1261 | CTGAACCTGTATTACTACACCATCTTCAACGAGACTTCGCGCTGCTTCCGAGGATC | 1320 | | | |
| OY | 1321 | CTGTGCGCGCCGTGGACCCAGACGGCTGTGTA | 1353 | | | |
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| DE | Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive; | | | | | |
| KW | hypertension; hypotensive; gene; ds. | | | | | |
| KX | Homo sapiens. | | | | | |
| OS | Key | | | | | |
| XX | Location/Qualifiers | | | | | |
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| XX | 13-FEB-2002; 2002WO-FI00113. | | | | | |
| XX | 20-FEB-2001; 2001FI-0000323. | | | | | |
| PR | (JURI-) JURILAB LTD OY. | | | | | |
| XX | Salonen J; | | | | | |
| XX | WPI; 2002-667063/71. | | | | | |
| PI | P-PSDB; AAE26634. | | | | | |
| DR | Detecting a risk of hypertension and targeting treatment in a subject | | | | | |
| XX | by determining the pattern of alleles encoding a variant | | | | | |
| PT | alpha-2-adrenoceptor | | | | | |
| XX | Disclosure; Page 27-29; 35pp; English. | | | | | |
| PS | The invention relates to a method for detecting a risk of hypertension | | | | | |
| XX | by determining the pattern of alleles encoding a variant alpha-2B- | | | | | |
| CC | adrenoceptor (AR) protein. The methods and compositions of the invention | | | | | |
| CC | are useful for detecting risks and targeting treatment for hypertension. | | | | | |
| CC | The kit is also useful for selecting for clinical drug trials testing | | | | | |
| CC | the antihypertensive effect of compounds. The present sequence is human | | | | | |
| CC | alpha-2B-adrenoceptor gene. | | | | | |
| CC | Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other; | | | | | |
| SO | Query Match | | | | | |
| OY | Best Local Similarity 99.9%; Score 1351.4; DB 24; Length 1353; | | | | | |
| DB | Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | | | | |
| 1 ATGAGCACACGAGACCCCTACTCTCGGTGACGACCAAGGCGCATPAGCGGCGCATCACCC 60 | | | | | | |
| 1 ATGAGCACACGAGACCCCTACTCTCGGTGACGACCAAGGCGCATPAGCGGCGCATCACCC 60 | | | | | | |

[illegible]

| | | | |
|----------|--|--|------|
| Db | 1141 | GTGCTCTGCTGGTTTCCCTTCTTCTTACGCTACAGCCCTGGGGCCGCACTGTGCCCAAGCAC | 1260 |
| Qy | 1201 | TGCAGGTGCCCCATGGCCCTCTTCCAGTTCTTTCTTGAGATCGGCTACCTGCAACAGCTCA | 1260 |
| Db | 1201 | TGCAAGGTGCCCCATGGCCCTCTTCCAGTTCTTTCTTGATCGGCTACTGCAACAGCTCA | 1260 |
| Qy | 1261 | CTGAACCCCTGTTATCTATACACCATCTTCAACCAAGAGACTTCGGCCGCTTCCGAGAGATC | 1320 |
| Db | 1261 | CTGAACCCCTGTTATCTATACACCATCTTCAACCAAGAGACTTCGGCCGCTTCCGAGAGATC | 1320 |
| Qy | 1321 | CTGTGCGCGCCGATGGAGCCAGACGGCCGTGTGA | 1353 |
| Db | 1321 | CTGTGCGCGCCGATGGAGCCAGACGGCCGTGTGA | 1353 |
| RESULT 4 | | | |
| ID | ACAS6583 | | |
| AC | ACAS6583 | standard, cDNA; 2072 BP. | |
| XX | ACAS6583; | | |
| XX | | | |
| DT | 06-JUN-2003 | (first entry) | |
| XX | | | |
| DE | Human signalling pathway polynucleotide probe SEQ ID NO 1181. | | |
| XX | | | |
| KW | Human; probe; ss; array element; Parkinson's disease; | | |
| KW | signalling pathway population; cancer; adenocarcinoma; leukaemia; | | |
| KW | immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray. | | |
| XX | | | |
| OS | Homo sapiens. | | |
| XX | | | |
| PN | US6500938-B1. | | |
| XX | | | |
| PD | 31-DEC-2002. | | |
| XX | | | |
| PE | 30-JAN-1998; 98US-0016434. | | |
| XX | | | |
| PR | 30-JAN-1998; 98US-0016434. | | |
| XX | | | |
| PA | (INCY-) INCYTE GENOMICS INC. | | |
| XX | | | |
| P1 | Au-Young J, Sellhammer JJ; | | |
| XX | | | |
| DR | WPI; 2003-352189/33. | | |
| XX | | | |
| PT | Combination of polynucleotide probes, useful as array elements in a | | |
| PT | microarray for monitoring the expression of a number of target | | |
| XX | polynucleotides | | |
| PS | Claim 1; SEQ ID NO 1181; 65bp; English. | | |
| XX | | | |
| CC | The invention relates to a combination which, comprises a number of | | |
| CC | polynucleotide probes comprising a sequence selected from one of the 1490 | | |
| CC | sequences mentioned in the specification. The combination is useful as an | | |
| CC | array element in a microarray for monitoring the expression of a number | | |
| CC | of target polynucleotides. The microarray is particularly useful in the | | |
| CC | diagnosis and treatment of cancer and immunopathology and neuropathology. | | |
| CC | The microarray is useful in diagnostics and treatment regimens, drug | | |
| CC | discovery and development, toxicological and carcinogenicity studies, | | |
| CC | forensics and pharmacogenomics. The microarray is also useful for | | |
| CC | monitoring progression of diseases and for developing sophisticated | | |
| CC | profiles for the effects of currently available therapeutic drugs. The | | |
| CC | combination is also useful for purifying a subpopulation of mRNAs, cDNAs | | |
| CC | and genomic fragments and in research and diagnostic applications. The | | |
| CC | array can detect changes in expression in a large number of genes coding | | |
| CC | for different signalling pathway populations which can be used to diagnose | | |
| CC | various diseases including cancer e.g. adenocarcinoma and leukaemia, | | |
| CC | immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease | | |
| CC | and Parkinson's disease. The present sequence represents a polynucleotide | | |
| CC | probe of the invention. | | |
| CC | Note: The sequence data for this patent did not form part of the printed | | |
| CC | specification but was obtained in electronic format directly from USPTO | | |

| CC | at | Seqdate | uniprot | gov/sequence | html?docID=065009303881 | | | | |
|----|-----------------------|---|---------|--------------|-------------------------|--------|--------|------|---|
| XX | Sequence | 2072 | Bp | 316 | A, 705 | C, 660 | G, 391 | T, 0 | other: |
| XX | Query Match | | | | | | | | 99.8%; Score 1349.8; DB 25; Length 2072; |
| XX | Best Local Similarity | | | | | | | | 99.9%; Pred. No. 4.1e-257; |
| XX | Matches 1351; | | | | | | | | Conservative 0; Mismatches 2; Indels 0; Gaps 0; |
| QY | 1 | ATGACACACAGAACCCCTACTCCGTGACAGGCCACAGCGGCATAGCGCGGCATCAC | 60 | | | | | | |
| DB | 413 | ATGACACACAGAACCCCTACTCCGTGACAGGCCACAGCGGCATAGCGCGGCATCAC | 472 | | | | | | |
| QY | 61 | TTCCCATCTCTTTACCATTTTGGGACAGCTCTGGTCAATCTGGCTGTGTTCACAGC | 120 | | | | | | |
| DB | 473 | TTCCCATCTCTTTACCATTTTGGGACAGCTCTGGTCAATCTGGCTGTGTTCACAGC | 532 | | | | | | |
| QY | 121 | CGCTGCTGCGCGCCCTCAGAACCTGTCTCTGTGTGCTGTGCGCGCGCGCATCTG | 180 | | | | | | |
| DB | 533 | CGCTGCTGCGCGCCCTCAGAACCTGTCTCTGTGTGCTGTGCGCGCGCGCATCTG | 592 | | | | | | |
| QY | 181 | GTGGCAGACTCATATCCCTTTTCTGCTGTGCCACAGAGACTGTGGCTACTGTACTTC | 240 | | | | | | |
| DB | 593 | GTGGCAGACTCATATCCCTTTTCTGCTGTGCCACAGAGACTGTGGCTACTGTACTTC | 652 | | | | | | |
| QY | 241 | CGGCGCACTGTGTGTGCGAGGTATACCTGGCGCTGCACTGTGCTCTTCTGCACTCTGTCATC | 300 | | | | | | |
| DB | 653 | CGGCGCACTGTGTGTGCGAGGTATACCTGGCGCTGCACTGTGCTCTTCTGCACTCTGTCATC | 712 | | | | | | |
| QY | 301 | GTGCACTGTGTGTGCGCATACAGCTGTGACCGGCTACTGTGGGCGGTGAGCGCGGCTGTGAGTAC | 360 | | | | | | |
| DB | 713 | GTGCACTGTGTGTGCGCATACAGCTGTGAGCGGCTACTGTGGGCGGTGAGCGCGGCTGTGAGTAC | 772 | | | | | | |
| QY | 361 | AACCTCAAGCGCACCCCGCGCGCATAGTGCATCATCTCACTGTGTGGCTCATCGCC | 420 | | | | | | |
| DB | 773 | AACCTCAAGCGCACCCCGCGCGCATAGTGCATCATCTCACTGTGTGGCTCATCGCC | 832 | | | | | | |
| QY | 421 | GCCTCATCTGTGCTGCGCGCCCTCATATPACAGGGCGACAGGGGCCCGCAGCGCGGG | 480 | | | | | | |
| DB | 833 | GCCTCATCTGTGCTGCGCGCCCTCATATPACAGGGCGACAGGGGCCCGCAGCGCGGG | 892 | | | | | | |
| QY | 481 | CGCCCCAGTGTGCAAGCTCAACAGAGAGCGGTGATATCCGTGGCTCAGATGTGATCT | 540 | | | | | | |
| DB | 893 | CGCCCCAGTGTGCAAGCTCAACAGAGAGCGGTGATATCCGTGGCTCAGATGTGATCT | 952 | | | | | | |
| QY | 541 | TTCTTTGCTCTTGGCTCATCATGATCTCTTGTCTTACCTGTGCGCATCTTACCTGTGCGCAAA | 600 | | | | | | |
| DB | 953 | TTCTTTGCTCTTGGCTCATCATGATCTCTTGTCTTACCTGTGCGCATCTTACCTGTGCGCAAA | 1012 | | | | | | |
| QY | 601 | CGACGCAACCGCAGAGGTCCAGAGGCGCAAGGGGGGGGCTGTGGCAGGGTGTGATCTCAAGCAG | 660 | | | | | | |
| DB | 1013 | CGACGCAACCGCAGAGGTCCAGAGGCGCAAGGGGGGGGCTGTGGCAGGGTGTGATCTCAAGCAG | 1072 | | | | | | |
| QY | 661 | CCCCGACCCCACTATGTGTGGGGCTTTTGGCTCAAGCCAACTGTGCCAGCCCTTGTGTG | 720 | | | | | | |
| DB | 1073 | CCCCGACCCCACTATGTGTGGGGCTTTTGGCTCAAGCCAACTGTGCCAGCCCTTGTGTG | 1132 | | | | | | |
| QY | 721 | GCTTCTGCGAGAGAGTCAACCGACACTCGAGTCCACTGTGGGAGAGAGAGAGGGGAG | 780 | | | | | | |
| DB | 1133 | GCTTCTGCGAGAGAGTCAACCGACACTCGAGTCCACTGTGGGAGAGAGAGAGGGGAG | 1192 | | | | | | |
| QY | 781 | ACCCCTGAGATACTGTGGGACCCCGGGCTTGTGCACCCAGTTGTGGCTGTGCTTCCCACTCA | 840 | | | | | | |
| DB | 1193 | ACCCCTGAGATACTGTGGGACCCCGGGCTTGTGCACCCAGTTGTGGCTGTGCTTCCCACTCA | 1252 | | | | | | |
| QY | 841 | GGCCAGGGCCAGAGAGAGGTGTTTTGTGGGCACTCTCAAGAGATGAAGCTGAAGAGAG | 900 | | | | | | |
| DB | 1253 | GGCCAGGGCCAGAGAGAGGTGTTTTGTGGGCACTCTCAAGAGATGAAGCTGAAGAGAG | 1312 | | | | | | |
| QY | 901 | GAAAGAGAGAGAGAGAGAGAGTGTGAACCCAGGAGAGTGCAGAGTCTCGGGCC | 960 | | | | | | |
| DB | 1313 | GAAAGAGAGAGAGAGAGAGAGTGTGTGAACCCAGGAGAGTGCAGAGTCTCTCGGGCC | 1372 | | | | | | |
| QY | 961 | TGACCTTGTGACGCCCGGCTGTGACAGACCAAGGGACTCCCGGCTGTGGCACTTACGT | 1020 | | | | | | |


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Db 999 CCGAGCAACCGCAGAGGTCCAGAGGCGCAAGGGGGGCTGGGAGGTGATCCAGCAG 1058
Oy 661 CCCCGACCCGACCATGATGGGGCTTTGGCTCAAGCCAACTGCAAGCCTGGCTGTGTG 720
Db 1059 CCCCGACCCGACCATGATGGGGCTTTGGCTCAAGCCAACTGCAAGCCTGGCTGTGTG 1118
Oy 721 GCTTCTCCAGAGAGGTCAACGACACTGGAAGTCACTGGGAGAGAGAGAGAGAGAGAG 780
Db 1119 GCTTCTCCAGAGAGGTCAACGACACTGGAAGTCACTGGGAGAGAGAGAGAGAGAG 1178
Oy 781 ACCCTGGAAGATCTGAGAACCCGGGGCTTGGCCACCCAGTGGGGCTCCCTCCCACTCA 840
Db 1179 ACCCTGGAAGATCTGAGAACCCGGGGCTTGGCCACCCAGTGGGGCTCCCTCCCACTCA 1238
Oy 841 GGCAGAGGCGCAGAGAGAGGTGTTTGTGGGCACTCTCAAGAGTGAAGCTGAAGAGAG 900
Db 1239 GGCAGAGGCGCAGAGAGAGGTGTTTGTGGGCACTCTCAAGAGTGAAGCTGAAGAGAG 1298
Oy 901 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 1299 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1358
Oy 961 TCAGCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 1359 TCAGCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1418
Oy 1021 GGCAGAGTGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1419 GGCAGAGTGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1478
Oy 1081 GGCAGAGTGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1479 GGCAGAGTGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1538
Oy 1141 GTGCTGTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
Db 1539 GTGCTGTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1598
Oy 1201 TGCAAGGTGCCCCAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
Db 1599 TGCAAGGTGCCCCAGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1658
Oy 1261 CTGAACCTGTTATCTACACCATCTTCAACCAAGAGACTTCGCGGTGCTCCGAGAGATC 1320
Db 1659 CTGAACCTGTTATCTACACCATCTTCAACCAAGAGACTTCGCGGTGCTCCGAGAGATC 1718
Oy 1321 CTGTGCGGCGCGTGAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353
Db 1719 CTGTGCGGCGCGTGAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1751

RESULT 7
AAT59499
ID AAT59499 standard; DNA; 2064 BP.
XX
AC AAT59499;
XX
AC 25-MAR-2003 (updated)
DT 06-MAY-1997 (first entry)
XX
DE Human alpha-2b adrenergic receptor genomic DNA clone.
XX
KW Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
KW epinephrine; signal transduction; neurotransmitter; ligand; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 288..1751
FT FT /*tag= a
XX
XX US5595880-A.
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PD 21-JAN-1997.
XX
PF 22-OCT-1992; 92US-0965040.
XX
PR 30-OCT-1989; 89US-0428856.
PR 30-MAY-1991; 91US-0707604.
PR 22-OCT-1992; 92US-0965040.
XX
PA (SYMA-) SYNAPTIC PHARM CORP.
XX
PI Hartig PR, Weinschenk RL;
XX
DR WPI; 1997-107576/10.
XX
DR P-PSDB; AAM11804.
XX
PT Assay for alpha-2b adrenergic receptor ligands - using membranes of
PT cells expressing recombinant receptor
XX
PS Disclosure; Fig 2A-E; 16pp; English.
XX
CC A genomic DNA clone (AAT59499) codes for human alpha-2b adrenergic
CC receptor (AAM11804), a member of the rhodopsin-like signal transducer
CC family. It was isolated from a human spleen genomic library in the
CC lambda vector Charon 28 by screening with a 1.6 kb fragment of the
CC human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B
CC comprising DNA encoding the alpha-2B adrenoceptor is deposited as
CC ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B
CC adrenoceptor in bacterial, yeast or mammalian cells; transfected
CC Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL
CC identify drugs which specifically interact with, and bind to, the
CC alpha-2b adrenergic receptor.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 2064 BP; 319 A; 636 C; 659 G; 390 T; 0 other;
XX
Query Match 98.3%; Score 1330.6; DB 18; Length 2064;
Best Local Similarity 99.0%; Pred. No. 2,5e-253;
Matches 1339; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Oy 1 AATGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 399 ATGAGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 458
Oy 61 TTCTCATCTCTTATACCATCTTGGCAAGCTGTGATCTCTGTGATCTGTGATCTGTGATCT 120
Db 459 TTCTCATCTCTTATACCATCTTGGCAAGCTGTGATCTCTGTGATCTGTGATCTGTGATCT 518
Oy 121 CGCTGCTGCGGCGCCCTCAGAACCTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 519 CGCTGCTGCGGCGCCCTCAGAACCTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 578
Oy 181 GTGGCCAGCTCATATATCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 579 GTGGCCAGCTCATATATCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 638
Oy 241 CGGCGCAGGTGAGAGAGGTGATCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db 639 CGGCGCAGGTGAGAGAGGTGATCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 698
Oy 301 GTGACACTGTGCGCCATCAAGCTTGACCGCTACTGAGCCGCTGAGAGATAC 360
Db 699 GTGACACTGTGCGCCATCAAGCTTGACCGCTACTGAGCCGCTGAGAGATAC 758
Oy 361 AATTCAGAGCGACCCCGCGCGCATCAAGTGTATCTCACTGTGTGTGTGTGTGTGTGTGTGT 420
Db 759 AATTCAGAGCGACCCCGCGCGCATCAAGTGTATCTCACTGTGTGTGTGTGTGTGTGTGTGT 818
Oy 421 GCGGTATCTGTGCGCGCCCTCATCTCAAGAGCGACAGAGCGCCCGCGCGCGCGCGCGCG 480
Db 819 GCGGTATCTGTGCGCGCCCTCATCTCAAGAGCGACAGAGCGCCCGCGCGCGCGCGCGCG 878
Oy 481 CGCCCCAGTGAAGTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATCT 540
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| Db | 879 | CGCCCCCAGTGCAGAGTCAACCAAGAGGCGCTGGTAACTCTGGCCCTTCAGCAATCGGATCT | 938 |
|--|------|---|------|
| OY | 541 | TTCTTTGCTCTTGCCCTCATCATGATCTTGTCTACCTGCGCATCTAACCCTGATGCGCAAA | 600 |
| Db | 939 | TTCTTTGGCTCTTGCCCTCATCATGATCTTGTCTACCTGCGCATCTAACCCTGATGCGCAAA | 998 |
| OY | 601 | CGCACCAACCGGAGAGGTCCTCCAGGGGCGCAAGGGGGGGGCTGGGCGAGGGTGAATCCAGACAG | 660 |
| Db | 999 | CGCACCAACCGGAGAGGTCCTCCAGGGGCGCAAGGGGGGGGCTGGGCGAGGGTGAATCCAGACAG | 105 |
| OY | 661 | CCCCACCCGACCACTAGTGGGGCTTTGGGCTCAGCCAACTGCGCACCCCTGGGCTCTGTG | 720 |
| Db | 1059 | CCCCACCCGACCACTAGTGGGGCTTTGGGCTCAGCCAACTGCGCACCCCTGGGCTCTGTG | 111 |
| OY | 721 | GCTTCTGCGAGAGAGTCAACCGGACCTTGAAATCTCACTGGGAGAGAGAGAGGGGGAG | 780 |
| Db | 1119 | GCTTCTGCGAGAGAGTCAACCGGACCTTGAAATCTCACTGGGAGAGAGAGAGGGGGAG | 117 |
| OY | 781 | AACCTTGAAAGATCTGGGACCCGGGGGCTTGCCACCAAGTTGGGCTGCTCTCCCACTCA | 840 |
| Db | 1179 | AACCTTGAAAGATCTGGGACCCGGGGGCTTGCCACCAAGTTGGGCTGCTCTCCCACTCA | 123 |
| OY | 841 | GCGCCAGGGCGAGAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG | 900 |
| Db | 1239 | GCGCCAGGGCGAGAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG | 129 |
| OY | 901 | GAAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAACCCCAAGCAGTGCAGTGTCTCCGGCC | 960 |
| Db | 1299 | GAAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAACCCCAAGCAGTGCAGTGTCTCCGGCC | 135 |
| OY | 961 | TCAGCTTGAGACCCCCCGCTGACAGACCAAGGGCTCCCGGGTGTGGCCACCTTACGT | 102 |
| Db | 1359 | TCAGCTTGAGACCCCCCGCTGACAGACCAAGGGCTCCCGGGTGTGGCCACCTTACGT | 141 |
| OY | 1021 | GCGCAGGTGCTCTGGGGCAGGGGGCGTGGGTGCTATAGTGGGCGAGTGGGCTGGAGG | 108 |
| Db | 1419 | GCGCAGGTGCTCTGGGGCAGGGGGCGTGGGTGCTATAGTGGGCGAGTGGGCTGGAGG | 147 |
| OY | 1081 | GCGCAGCTGACCCCGGAGAGAGCGCTTCACTTCTGTGCTGGCTGTGCTCAATGGCGTTTTT | 114 |
| Db | 1479 | GCGCAGCTGACCCCGGAGAGAGCGCTTCACTTCTGTGCTGGCTGTGCTCAATGGCGTTTTT | 153 |
| OY | 1141 | GTCGCTGCTGCTGCTTCCCTCTTCTTCTTCAAGCTACAGCTTGGGGCGCATCTGCCGAAGCAC | 120 |
| Db | 1539 | GTCGCTGCTGCTGCTTCCCTCTTCTTCTTCAAGCTACAGCTTGGGGCGCATCTGCCGAAGCAC | 159 |
| OY | 1201 | TGCAGAGTGGCCCAATGGGCTCTTCCAGTTCCTTCTGGAATGGGCTAATGGAACAGCTCA | 126 |
| Db | 1599 | TGCAGAGTGGCCCAATGGGCTCTTCCAGTTCCTTCTTCTGGAATGGGCTAATGGAACAGCTCA | 165 |
| OY | 1261 | CTGAACCCCTGATATCTACACATCTTCAACACAGAACTTCCGCGGTGCTTCCGAGAGATC | 132 |
| Db | 1659 | CTGAACCCCTGATATCTACACATCTTCAACACAGAACTTCCGCGGTGCTTCCGAGAGATC | 171 |
| OY | 1321 | CTGTGCGGCGCCGTGAGCCCAAGCGGCTGTGA | 1353 |
| Db | 1719 | CTGTGCGGCGCCGTGAGCCCAAGCGGCTGTGA | 1751 |
| RESULT 8 | | | |
| AA199906 | | | |
| AA199906 standard; DNA; 1344 BP. | | | |
| AA199906; | | | |
| 18-FEB-2002 (first entry) | | | |
| Human alpha-2BAR third intracellular loop variant encoding DNA. | | | |
| Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; | | | |
| polymorphic site; allelic variant; cardiovascular disease; | | | |
| central nervous system disease; adenylyl cyclase; MAP kinase activity; | | | |

phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.

Homo sapiens.

| Key | Location/Qualifiers |
|--------|---|
| FT CDS | 1..1344 |
| FT | /*tag= a |
| FT | /product= "alpha-2BAR" |
| FT | /note= "sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909 of the wildtype alpha-2BAR protein (AA199905)" |

MO200179561-A2.

25-OCT-2001.

17-APR-2001; 2001WO-US12575.

17-APR-2000; 2000US-0551744.

10-AUG-2000; 2000US-0636259.

19-OCT-2000; 2000US-0692077.

(LIGG/) LIGGETT S B.

(SMAL/) SMALL K M.

Liggett SB, Small KM,

WPI; 2001-611728/70.

P-PSDB; AAM52118.

Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -

Claim 5; Page 144-145; 163pp; English.

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising:

(a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A or alpha2C or fragment or complement of; and

(b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (A) (ggggcgggcg) or (B) (ggggcggtgag) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239, rauwolficine, idazoxan, tolazoline, phenolamine and combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the third intracellular loop of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909 of the wildtype gene (AA199905).

Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;

Query Match 97.9%; Score 1325; DB 23; Length 1344;

Best Local Similarity 99.3%; Pred. No. 3e-252;

Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

1 ATGACACACAGAGCCCTACTCGGTACAGGCCACAGCGGCATATGCGGGGCATACCC 60

1 ATGACACACAGAGCCCTACTCGGTACAGGCCACAGCGGCATATGCGGGGCATACCC 60

QY 61 TTCTCATTTCTTTTACCATCTTGGCAAGCTGTGCTCATCTGAGCTGTGTTGACAGC 120
 Db 61 TTCTCATTTCTTTTACCATCTTGGCAAGCTGTGCTCATCTGAGCTGTGTTGACAGC 120
 QY 121 CGCTGCTGCGGCGCCCTTCAGAACCTGTTCCTGTGCTGCTGCGCGCGCGAGCATCTG 180
 Db 121 CGCTGCTGCGGCGCCCTTCAGAACCTGTTCCTGTGCTGCTGCGCGCGCGAGCATCTG 180
 QY 181 GTGGGACAGCTCATCTATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 Db 181 GTGGGACAGCTCATCTATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 241 CGGCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 Db 241 CGGCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 QY 301 GTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 Db 301 GTGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 361 AACTCCAGGCGCACCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Db 361 AACTCCAGGCGCACCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 421 GCGGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Db 421 GCGGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 481 CGGCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 Db 481 CGGCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 541 TTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 Db 541 TTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 541 TTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 Db 541 TTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 601 CGGCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 Db 601 CGGCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 661 CGGCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Db 661 CGGCGGACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 721 GCTTCTGCGAGAGGTCAACGAGCACTGCAAGTCACTGCGAGAGAGAGAGAGAGAG 780
 Db 721 GCTTCTGCGAGAGGTCAACGAGCACTGCAAGTCACTGCGAGAGAGAGAGAGAGAG 780
 QY 781 ACCCTGGAAGATCTTGGGACCGGCGCTGCGGCAAGTGGGCTGCTTCCAACTCA 840
 Db 781 ACCCTGGAAGATCTTGGGACCGGCGCTGCGGCAAGTGGGCTGCTTCCAACTCA 840
 QY 841 GGCAGGCGCAG 900
 Db 841 GGCAGGCGCAG 900
 QY 841 GGCAGGCGCAG 891
 Db 841 GGCAGGCGCAG 891
 QY 901 GAAG 960
 Db 901 GAAG 960
 QY 992 TCACTTGTGCAAGCCCGCGCTGCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1011
 Db 992 TCACTTGTGCAAGCCCGCGCTGCGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1011
 QY 1021 GGCAGGAGTCTCTGCGAG 1080
 Db 1021 GGCAGGAGTCTCTGCGAG 1080
 QY 1012 GGCAGGAGTCTCTGCGAG 1071
 Db 1012 GGCAGGAGTCTCTGCGAG 1071
 QY 1081 GGCAGGAGTCTCTGCGAG 1140
 Db 1081 GGCAGGAGTCTCTGCGAG 1140
 QY 1072 GGCAGGAGTCTCTGCGAG 1131
 Db 1072 GGCAGGAGTCTCTGCGAG 1131
 QY 1141 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
 Db 1141 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200

Db 1132 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1191
 QY 1201 TCGAAGTGTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
 Db 1192 TCGAAGTGTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1251
 QY 1261 CTGAAGCTGTGATCTTCAACCATCTTCAACGAGACTTCCGCGCTGCTGCTGCTG 1320
 Db 1252 CTGAAGCTGTGATCTTCAACCATCTTCAACGAGACTTCCGCGCTGCTGCTGCTG 1311
 QY 1321 CTGTCGCGCGCGCTGAGACCCAGACGCGCTGCTGTA 1353
 Db 1312 CTGTCGCGCGCGCTGAGACCCAGACGCGCTGCTGTA 1344
 RESULT 9
 AAD04761
 ID AAD04761 standard; DNA; 1344 BP.
 AC AAD04761;
 DT 04-JUL-2001 (first entry)
 XX
 DE Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
 KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Primmetal's variant; ds.
 XX
 OS Homo sapiens.
 FH Key
 FT 1.1344
 FT CDS /tag= a
 FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
 FT /variant protein"
 PN W0200129082-A1.
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000WO-FI00913.
 XX
 PR 22-OCT-1999; 99US-0422985.
 XX
 PA (JUVA-) JUVANTIA PHARMA LTD OY.
 XX
 PI Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
 PI Schelin M, Salonen JT, Tuominen T, Lakka TA, Nyyssönen K;
 PI Salonen R, Kaunonen J, Valkonen V;
 XX
 DR WPI: 2001-300318/31.
 DR P-PSDB; AAE00989.
 XX
 FT New DNA molecule encoding variant specific adrenoceptor protein with
 FT deletion of specific amino acids located in the third intracellular
 FT loop of the polypeptide, for treating vascular contraction of coronary
 FT arteries
 PS Claim 3; Page 24-26; 37pp; English.
 XX
 CC The present sequence is a gene encoding human alpha2B-adrenoceptor
 CC (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
 CC element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
 CC 18 amino acids (amino acids 294-311), located in the third intracellular
 CC loop of the receptor polypeptide. The variant is obtained by deletion of
 CC three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
 CC gene is located on chromosome 2. Alpha2-AR mediate many of the
 CC physiological effects of the catecholamines, norepinephrine and
 CC epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating

CC a mamma_suffering from vascular contraction of coronary arteries and a
CC disease_involving vascular contraction of coronary arteries which is
CC clinically expressed as coronary heart disease (CHD), unstable chronic
CC angina pectoris which is clinically expressed as Prinzmetal's variant
CC form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
CC gene therapy.

SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;

| Query Match | 97.88; | Score 1323.4; | DB 22; | Length 1344; |
|-------------|--------|---------------|--------|--------------|
| Post 10001 | 90.38; | Score 1323.4; | DB 22; | Length 1344; |

Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

| | | | |
|----|-----|--|-----|
| Qy | 1 | ATGAGCAACAGAGACCCCTACTCCGTGCAGAGGCACAGCGGCAATACCGGCGGCATACAC | 60 |
| Db | 1 | ATGAGCAACAGAGACCCCTACTCCGTGCAGAGGCACAGCGGCAATACCGGCGGCATACAC | 60 |
| Qy | 61 | TTCCATATTCCTTTAACCATCTTCGGACAAGCTCTGGTCACTCTGGCTGTGTGACACAG | 120 |
| Db | 61 | TTCCATATTCCTTTAACCATCTTCGGACAAGCTCTGGTCACTCTGGCTGTGTGACACAG | 120 |
| Qy | 121 | GGCTGCATGCGCGCCCTCAGAAACCTGTTCCTGGTGTCTGCTGGCCGCGCCGACATCCCTG | 180 |
| Db | 121 | GGCTGCATGCGCGCCCTCAGAAACCTGTTCCTGGTGTCTGCTGGCCGCGCCGACATCCCTG | 180 |
| Qy | 181 | GTGGCGACGCTCATCATCCCTTTCCTGCTGGCCAAAGACCTGCTGGGCTTAAGTGTACTTC | 240 |
| Db | 181 | GTGGCGACGCTCATCATCCCTTTCCTGCTGGCCAAAGACCTGCTGGGCTTAAGTGTACTTC | 240 |
| Qy | 241 | CGGGCGACGTGGTGGAGAGTGTAACTCTGGGGCTCGAAGTCTCTTCTGCACTCTGCTCATCT | 300 |
| Db | 241 | CGGGCGACGTGGTGGAGAGTGTAACTCTGGGGCTCGAAGTCTCTTCTGCACTCTGCTCATCT | 300 |
| Qy | 301 | GTGCACCTGTGGCGCATCAGCTGTGACCCGCTACTGGGGCGTAGACCGCCGCTGAGATAC | 360 |
| Db | 301 | GTGCACCTGTGGCGCATCAGCTGTGACCCGCTACTGGGGCGTAGACCGCCGCTGAGATAC | 360 |
| Qy | 361 | AACTTCAGAGCGCAACCCCGCGCGCATCAAGTGATCATCTCTACTGTGGCTCATTCGCC | 420 |
| Db | 361 | AACTTCAGAGCGCAACCCCGCGCGCATCAAGTGATCATCTCTACTGTGGCTCATTCGCC | 420 |
| Qy | 421 | GGCGCATCTGGCTGCGCGCCCTCATCTTCAAGAGGGGACAAGAGGACCCCGACCGCGCGGG | 480 |
| Db | 421 | GGCGCATCTGGCTGCGCGCCCTCATCTTCAAGAGGGGACAAGAGGACCCCGACCGCGCGGG | 480 |
| Qy | 481 | CGCCCCAGTGCAGACTCAACACAGAGGGCTGTGTACATCTGGCCCTCCAGCATCCGATCT | 540 |
| Db | 481 | CGCCCCAGTGCAGACTCAACACAGAGGGCTGTGTACATCTGGCCCTCCAGCATCCGATCT | 540 |
| Qy | 541 | TTCTTTTGCTCTTGCGCTCATATGATCCTTGTCTTACTTGGCATCTAACCTGATCGCAAA | 600 |
| Db | 541 | TTCTTTTGCTCTTGCGCTCATATGATCCTTGTCTTACTTGGCATCTAACCTGATCGCAAA | 600 |
| Qy | 601 | CGACGCAACCGCAGAGGTCCACAGGCGCAAGAGGGGGGCTGGGCAAGGTAAGTCCAAAGCAG | 660 |
| Db | 601 | CGACGCAACCGCAGAGGTCCACAGGCGCAAGAGGGGGGCTGGGCAAGGTAAGTCCAAAGCAG | 660 |
| Qy | 661 | CCCGGACCCGACCATGTGTGGGGCTTTGGCTCAGCCAACTGCGACGCCCTGTGGCTGTG | 720 |
| Db | 661 | CCCGGACCCGACCATGTGTGGGGCTTTGGCTCAGCCAACTGCGACGCCCTGTGGCTGTG | 720 |
| Qy | 721 | GCTTCTGCAGAGAGGTCAACGGAACCTGGAAGTCCACTGGGGAGGAAGAGAGGGGGAG | 780 |
| Db | 721 | GCTTCTGCAGAGAGGTCAACGGAACCTGGAAGTCCACTGGGGAGGAAGAGAGGGGGAG | 780 |
| Qy | 781 | ACCCCTGAAGATCTGGGACCCGGGCTTTGGCCACCAAGTGTGGGCTGCGCTTCCCACTCA | 840 |
| Db | 781 | ACCCCTGAAGATCTGGGACCCGGGCTTTGGCCACCAAGTGTGGGCTGCGCTTCCCACTCA | 840 |
| Qy | 841 | GGCCAGGGGCAAGAGAGGGGTTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG | 900 |
| Db | 841 | GGCCAGGGGCAAGAGAGGGGTTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG | 900 |

| | | | |
|----|------|---|------|
| QY | 901 | GAAAGAGAGAGAGAGAGAGAGAAAGATGTGAACCCAGAGGACGTGCACAGTGTCTCCGAC | 960 |
| Db | 901 | GAAAGAGAGAGAGAG-----GAGTGTGAACCCAGGACAGTGCACAGTGTCTCCGACC | 951 |
| QY | 961 | TCAGCTTGACAGCCCCCGCTGACAGACCCACAGGAGCTCCCGAGTGTGGCCACCTTACGT | 1020 |
| Db | 952 | TCAGCTTGACAGCCCCCGCTGACAGACCCACAGGAGCTCCCGAGTGTGGCCACCTTACGT | 1011 |
| QY | 1021 | GGCCAGGAGCTCTCGGCGACAGGAGGAGTGGAGTCTAAGTGGGCGAGTGTGGCGTCCAAAG | 1080 |
| Db | 1012 | GGCCAGGAGCTCTCGGCGACAGGAGGAGTGGAGTCTAAGTGGGCGAGTGTGGCGTCCAAAG | 1071 |
| QY | 1081 | GCGCAGCTGAACCCGAGAGAAAGCGCTTACCTTCGTGCTGAGCTGTGATTCATTGGCGTTT | 1140 |
| Db | 1072 | GCGCAGCTGAACCCGAGAGAAAGCGCTTACCTTCGTGCTGAGCTGTGATTCATTGGCGTTT | 1131 |
| QY | 1141 | GTCGCTGCTGCTGTTCCTCTTCTTCTTCAAGCTACAGCTGGGCGCGCATCTGCGGAGACAC | 1200 |
| Db | 1132 | GTCGCTGCTGCTGTTCCTCTTCTTCTTCAAGCTACAGCTGGGCGCGCATCTGCGGAGACAC | 1191 |
| QY | 1201 | TGCAAGGTGCCCATGAGGCTCTTCCAGTCTCTTCTTGATTCGGCTACTGCAACAGCTCA | 1260 |
| Db | 1192 | TGCAAGGTGCCCATGAGGCTCTTCCAGTCTCTTCTTGATTCGGCTACTGCAACAGCTCA | 1251 |
| QY | 1261 | CTGAACCTGTATTCTACACCATCTTCAACCGAGACTTCGCGCGTGCCTTCCGAGATC | 1320 |
| Db | 1252 | CTGAACCTGTATTCTACACCATCTTCAACCGAGACTTCGCGCGTGCCTTCCGAGATC | 1311 |
| QY | 1321 | CTGTGCGCGCCGCTGAGACCCAGAGGCGCTGGTGA | 1353 |
| Db | 1312 | CTGTGCGCGCCGCTGAGACCCAGAGGCGCTGGTGA | 1344 |

RESULT 10

ID AAD44388 standard; DNA; 1344 BP.

AC AAD44388;

DT 13-DEC-2002 (first entry)

Human alpha-2B-adrenoceptor variant DNA.

KW hypertension: variant: gene: *rs*
 KW human; hypertension; alpha-2b-adrenoceptor; AR; antihypertensive;

05 Homo sapiens.

XX

| | | |
|----|-----|---------|
| FT | CDS | 1..1344 |
|----|-----|---------|

| FT | product= "Human alpha-2B-adrenoceptor variant |
|----|---|
| FT | |

XX
DN W0300266617-21

AA PD 29-AUG-2002.

13-FEB-2002; 2002WO-FI00113.

PR 20-FEB-2001; 2001FI-0000323.

PA (JURI-) JURILAB LTD OY.

PI Salonen J
vv

DR WP1; 2002-667063/71.
DR P-PSDB: AAE26633

PT Detecting a risk

PT alpha-2-adrenoceptor -

Db 781 ACCCCTGAGATACTGGGACCGGGCTTTGCCACCCAGTTGGGCTGCCCTTCCCAATCA 8

[illegible]

QY 241 CGGCGCAGTGGTGCAGAGGTGTAAGTGGGCTGAGACCTGCTCTTCTGCACTTCGTCATC 300
 DB 5241 CGGCGTACCGTGGCCAGAGGTGTAATGGGCTTCGACGTGTTTGTGTAATTCGTTTATC 5300
 QY 301 GTGGCACTGTGGCCCTCAAGCCCTGACCCCTACTGGCCGTGAGCCCGCGCTGAGTAC 360
 DB 5301 GTGTATTTGTGCTTATGTTGATGATGCTTATTTGGGTGATGCTGCGGTGGAGTAT 5360
 QY 361 AACTCCAGACGACCCCGCGCATCAAGTGCATCATCTCTACTGTGAGCTCATCGCC 420
 DB 5361 AATTTTAAACGTAATTCGCGGTGTAATGATGTAATTTTATTTGATGCTTATTCGTC 5420
 QY 421 GCGGTATCTGCTGCGCCCTCATCTCAAGAGGCGACAGGCGCCCAAGCCCGCGCGG 480
 DB 5421 GTGCTATTTGCTGTGCTGTTTATTTATTAAGGCGATTAAGGCTTTTATAGTGGCGCGG 5480
 QY 481 CGCCCCCATGCAAGCTCAACAGAGGCGCTGTAATCTGCGCTCCAGCATCGATCT 540
 DB 5481 CGTTTATGTAAGTTTATTAATTAAGAGGCTTGGTATATTTGTTTATGTAATCGATTT 5540
 QY 541 TTTCTTGTCTCTGCTCATCATGATCTGTCTACCTGCGCATCTACCGTATCGCCAA 600
 DB 5541 TTTTGTGTTTGTGTTTATTTATGATTTTGTGTTTATTTGCGTATTTATTTGATCGTTAA 5600
 QY 601 CGCAGCAACCGAGAGGTCCAGGCGCAAGGCGGCGCTGGCGAGGTGATCCAGCAG 660
 DB 5601 CGTATGATCGTAGAGGTTTATAGGCTTAAAGGCGGCTTGGTAAAGGCTTAAGTAA 5660
 QY 661 CCCCAGCCGACCAATGTGTGGGCTTTGGCTCAGCCAACTGCGACCCCTGCTCTGTG 720
 DB 5661 TTTCAATTCGATTAATGTTGGGCTTTGTTGTTTATGTTAAATTTGTTTGTGTTTGTG 720
 QY 721 GCTTCGCGAGAGGTCAACGAGCACTGAGAGTCCACTGGGAGAGAGAGAGAGAGAG 780
 DB 5721 GTTTTGTATGAGAGGTTAAAGGATTTGAGAGTTTATTTGGGAGAGAGAGAGAGAGAG 5780
 QY 781 ACCCTGAGAGATCTGGGACCCGCGCTTGGCCACCCAGTTGGGCTGCTCCCACTCA 840
 DB 5781 AATTTTGAAGATATTCGGAATTCGGGCTTTGTTATTTAGTTAGTTGTTTATTTATTTA 5840
 QY 841 GCGCAGGCGCAGAGAGGTTGTTTGGGGCACTCCAGAGAGTGAAGCTGAAGAGAG 900
 DB 5841 GGTGAGGTTTAAAGAGAGGTTGTTGTTGGGCTATTTTGAAGATGAAAGTT----- 5891
 QY 901 GAAAG 960
 DB 5892 GAAAG 5951
 QY 961 TCAGCTTGCAGCCCGCTGCGAGCAGCAGAGGCTCCGCGG 1003
 DB 5952 TTAGTTTGTATGTTTTCGTTGTTAGTATGTTATAGGCTTTTCGGG 5994
 RESULT 14
 AAD28364
 ID AAD28364 standard; DNA; 6904 BP.
 XX
 AC AAD28364;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Human chemically treated genomic DNA #5.
 XX
 KM Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
 KM adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
 KM behavioral disorder; neurological; psychiatric; cancer; schizophrenia;
 KM Tourette's syndrome; smoking; human immunodeficiency virus dementia;
 KM drug abuse; migraine; de.
 XX
 OS Homo sapiens.
 XX
 PN WO200202809-A2.
 XX

PD 10-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-BP07540.
 XX
 PR 30-JUN-2000; 2000DE-1032529.
 XX
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIS-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-154759/20.
 XX
 PT Novel nucleic acid useful for diagnosis and therapy of behavioral
 PT disorder, neurological disorder and cancer, comprises a sequence of a
 PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
 PT gene -
 XX
 PS Claim 1; Page 40-44; 190pp; English.
 XX
 CC The invention relates to nucleic acids comprising a segment of chemically
 CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
 CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
 CC useful for detecting cytosine methylations. The pretreated DNA is useful
 CC for the diagnosis or therapy of behavioural disorders, neurological
 CC disorders and cancer, in particular major depressive disorder, Tourette's
 CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
 CC drug abuse, alcoholism, personality traits, compulsive gambling, human
 CC immunodeficiency virus dementia, migraine, behaviour in schizophrenia
 CC and schizoaffective patients, and suicidal behaviour in patients with
 CC schizophrenia. The nucleic acid is useful for detecting the methylation
 CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
 CC (SNPs). The present sequence is human chemically treated genomic DNA.
 XX
 SQ Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 1 other;
 Query Match 37.9%; Score 512.6; DB 24; Length 6904;
 Best Local Similarity 70.3%; Pred. No. 7-5e-92;
 Matches 705; Conservative 0; Mismatches 289; Indels 9; Gaps 1;
 QY 1 ATGACCAACAGAGACCCCTACTCTCGTGAGGCGACAGCGGCATAGCGGCGCATCACC 60
 DB 5001 ATGATATTATTAAGATTTTATTTATTCGATGATTAAGCGATTATAGCGCGTTATTATT 5060
 QY 61 TTCCTATCTCTTATACATCTTCGCAACGCTGTGTATCTGCTGTGTGACACG 120
 DB 5061 TTTTATTTATTTTATTAATTTTCGTTACGTTTGGTATATTTGTTGTTGATTAGT 5120
 QY 121 CGCTGCTGCGCGCCCTCAGAACCTGTTCTGTGTGTGCTGCGCGCGCGCGCATCTCG 180
 DB 5121 CGTTGCTGCGCGCTTTTATTAATTTTATTTGTTGTTGTTGTTGTTGTTGTTGTTG 5180
 QY 181 GTGGCAGCGCTCATATCCCTTTCTGCTGCGCAACGAGCTGCGGCTACTGTACTTC 240
 DB 5181 GTGTTAGTTATTAATTTTATTTTTCGTTGTTAAGAGTTGTGGGTTATTTGATTTT 5240
 QY 241 CGGCGCAGTGTGTGAGAGGTGTAAGTGTGCTGACAGTCTCTTCTGCACTTCGTCATC 300
 DB 5241 CGGCGTACGTTGTGCGAGAGGTGTAATTTGGGCTTGAAGTGTGTTTGTATTTCTTTATC 5300
 QY 301 GTGGCACTGTGCGCATGAGCTGAGACGCTAAGGCGCGTACGCGCGCGCGAGTAC 360
 DB 5301 GTGTATTTGTGCTTATTAATTTGATGATGCTTATTTGATGCTTATTTGATGCTTATTC 5360
 QY 361 AACTCCAGACGACCCCGCGCATCAAGTGCATCATCTCTACTGTGAGCTCATCGCC 420
 DB 5361 AATTTTAAACGTAATTCGCGGTGTAATGATGTAATTTTATTTGATGCTTATTCGTC 5420
 QY 421 GCGGTATCTGCTGCGCCCTCATCTCAAGAGGCGACAGGCGCCCAAGCCCGCGCGG 480
 DB 5421 GTGCTATTTGCTGTGCTGTTTATTTATTAAGGCGATTAAGGCTTTTATAGTGGCGCGG 5480
 QY 481 CGCCCCCATGCAAGCTCAACAGAGGCGCTGTAATCTGCGCTCCAGCATCGATCT 540

DB 550 TTCCCGCCGCTGCTCT---CGCTTACCCGCCAGCCCGACGCGCGCCCTTACCCGCGAGTGC 606
QY 493 AAGCTCAACAGAGGCGCTGTACATCCGAGCCTCCAGCATCGGATCTTCTTTGCTCT 552
DB 607 GGCCTTCAAGACGAGACTGTGTACATCTGTCTCTCTGTGATCGGCTCTTTCGCGCC 666
QY 553 TGCCTCATCATGATCCTTGTCTTACCTGCGCATCTTACCTGTATCGCCAAACGACAAACCGC 612
DB 667 TGCCTCATCATGAGCCTGTGTCTACGCGCGCATCTTACGAGTGGCCAAAGCGTGCACGCGC 726
QY 613 AAGAGTCCAGGCGCCAAAGGCGCGCGCTGCGCGAGGTAGTCCAAAGCAGCCCGACCGAC 672
DB 727 A-----CGCTCAGCAGAAAGCGCGCCCGGTGCGCGCCGACGAGTGCCTCCGAC 776
QY 673 CATGTGCGGCGCTTTGGCCTCAGCCAAACTGCCAGCCCTGCGCTCTGTGCTTCTGCCAGA 732
DB 777 TACCG-----AAAAAGGCTGAGCGCGCGCGCGCAGCGCAGAGCGAGAAC 818
QY 733 GAGGTCAACGAGCACTCGAAGTCACTGCGGAGAAAGAGAGGCGGAGACCCCTGAAGAT 792
DB 819 GGGCACTGCGCGCCCGCCCGCGCGCGCGAGCTGAGCCGAGACGAGCAGCGCAGCGCGAG 878
QY 793 ACTGCGACCCGCGCGCTTGCACCCAGTTGAGGCTGCCCTTCCCACTCAGCGCAGCGCAG 852
DB 879 AGCGCG-----CG 903
QY 853 AAGGAGGCTGTTGTGCGGCGATCTCCAGAGATGAAGCTGAAGAGAGAGAGAGAGAG 912
DB 904 CGGCG 963
QY 913 GAGGAGAGAGAGAGAGTGAACCCCAAGGAGTGCAGTGTCTCCGCGCTCAGCTTGCAGC 972
DB 964 GCG 1023
QY 973 CCCCGCTGCACAGCCACAGGAGCTCCCGGCTGCTGCGCACCTTACGTGCGCAGGTGCTC 1032
DB 1024 GCGCGCGCTTCTCGCGCGCGCGAGCTCGCGCTCGTGAAGTCTTCTGTGCGCGCGCGCG 1083
QY 1033 CTGGGCAAGGCGCGTGGGTCTTAAAGTGGGCAAGTGTGCGCTGCAAGGCGCGAGCTGACC 1092
DB 1084 GCGCGCAGCAGCGT-----GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1122
QY 1093 CGGAGAGAGCGCTTCACTTCTGAGCTGAGTGTGATCTTGGGCTTTTGTGCTGTGCG 1152
DB 1123 CGCGAGAGCGCTTCACTTGTGTGCTGAGTGTGATGAGCGTGTTCGTGCTGTGCG 1182
QY 1153 TTCCCTTCTTCTTCACTACAGCCCTGCGCGCATCTGCGCGAGCACTGCAAGGTGCC 1212
DB 1183 TTCCCTTCTTCTTCACTACAGCGCTGTACGCGATCTGCGCGAGCGCTGCCAGGTGCC 1242
QY 1213 CATGCGCTTCTTCAAGTCTTCTTCTGAGTGCAGTACCTGCAACAGCTCACTGAACCTGTT 1272
DB 1243 GCGCGCGCTTCAAGTCTTCTTCTGAGTGCAGTACCTGCAACAGCTCGCTCAACCGGTC 1302
QY 1273 ATCTACACATTTTCAACAGAGACTTCCGCGCTTCCGAGAGATCTGTGCGCGCG 1332
DB 1303 ATCTACACAGCTTCAACAGAGATTTCCGCGCATCTTCAACAGCATCTTCCGAGCG 1362
QY 1333 TGA 1336
DB 1363 AGGA 1366

Search completed: February 7, 2004, 20:50:52
Job time : 404.318 secs

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:26:52 ; Search time 89.7987 Seconds
(without alignments)
6650.337 Million cell updates/sec

Title: US-09-692-077D-1

Perfect score: 1353
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 563978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/prodata/2/ina/PCFUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------------------|-------------------|
| 1 | 1349.8 | 99.8 | 2072 | 4 US-09-016-434-1181 | Sequence 1181, Ap |
| 2 | 430 | 32.8 | 1382 | 4 US-09-016-434-1256 | Sequence 1256, Ap |
| 3 | 430 | 31.8 | 3604 | 4 US-09-016-434-1180 | Sequence 1180, Ap |
| 4 | 184.8 | 13.7 | 3335 | 1 US-07-676-174A-1 | Sequence 1, Appl |
| 5 | 163.4 | 12.1 | 3335 | 1 US-08-194-338-1 | Sequence 1, Appl |
| 6 | 158.6 | 11.7 | 921 | 1 US-08-722-001-17 | Sequence 17, Appl |
| 7 | 158.6 | 11.7 | 1567 | 1 US-08-722-001-24 | Sequence 24, Appl |
| 8 | 157 | 11.6 | 1738 | 1 US-08-334-698-3 | Sequence 3, Appl |
| 9 | 157 | 11.6 | 1738 | 1 US-08-228-932-3 | Sequence 3, Appl |
| 10 | 157 | 11.6 | 1738 | 1 US-08-468-939-3 | Sequence 3, Appl |
| 11 | 157 | 11.6 | 1738 | 2 US-08-406-855A-3 | Sequence 3, Appl |
| 12 | 157 | 11.6 | 1738 | 2 US-08-722-001-3 | Sequence 3, Appl |
| 13 | 157 | 11.6 | 1738 | 3 US-08-244-354-3 | Sequence 3, Appl |
| 14 | 157 | 11.6 | 1738 | 3 US-09-206-899-3 | Sequence 3, Appl |
| 15 | 157 | 11.6 | 1738 | 4 US-09-444-783-3 | Sequence 3, Appl |
| 16 | 157 | 11.6 | 1738 | 4 US-09-688-415-3 | Sequence 3, Appl |
| 17 | 157 | 11.6 | 1738 | 4 US-09-016-434-1402 | Sequence 1402, Ap |
| 18 | 157 | 11.6 | 1738 | 5 PCT-US95-04203-3 | Sequence 1402, Ap |
| 19 | 149.6 | 11.1 | 1621 | 1 US-08-722-001-13 | Sequence 13, Appl |
| 20 | 149.6 | 11.1 | 1776 | 1 US-08-722-001-29 | Sequence 29, Appl |
| 21 | 149.6 | 11.1 | 2002 | 4 US-09-016-434-1172 | Sequence 1172, Ap |
| 22 | 149.6 | 11.1 | 2140 | 1 US-08-334-698-1 | Sequence 1, Appl |
| 23 | 149.6 | 11.1 | 2140 | 1 US-08-228-932-1 | Sequence 1, Appl |
| 24 | 149.6 | 11.1 | 2140 | 1 US-08-468-939-1 | Sequence 1, Appl |
| 25 | 149.6 | 11.1 | 2140 | 2 US-08-406-855A-1 | Sequence 1, Appl |
| 26 | 149.6 | 11.1 | 2140 | 2 US-08-722-190-1 | Sequence 1, Appl |
| 27 | 149.6 | 11.1 | 2140 | 3 US-08-244-354-1 | Sequence 1, Appl |

| | | | | | |
|----|-------|------|------|----------------------|-------------------|
| 28 | 149.6 | 11.1 | 2140 | 3 US-09-206-899-1 | Sequence 1, Appl |
| 29 | 149.6 | 11.1 | 2140 | 4 US-09-444-783-1 | Sequence 1, Appl |
| 30 | 149.6 | 11.1 | 2140 | 4 US-09-688-415-1 | Sequence 1, Appl |
| 31 | 149.6 | 11.1 | 2140 | 5 PCT-US95-04203-1 | Sequence 1, Appl |
| 32 | 139.8 | 10.3 | 1601 | 1 US-08-722-001-7 | Sequence 7, Appl |
| 33 | 139.8 | 10.3 | 1997 | 1 US-08-722-001-27 | Sequence 27, Appl |
| 34 | 139.8 | 10.3 | 2004 | 1 US-08-722-001-11 | Sequence 11, Appl |
| 35 | 138.4 | 10.2 | 1930 | 4 US-09-016-434-1171 | Sequence 1171, Ap |
| 36 | 138.4 | 10.2 | 2463 | 1 US-08-370-542-1 | Sequence 1, Appl |
| 37 | 138.4 | 10.2 | 2463 | 1 US-08-542-358-1 | Sequence 1, Appl |
| 38 | 138.4 | 10.2 | 2463 | 3 US-09-018-351-1 | Sequence 1, Appl |
| 39 | 138.2 | 10.2 | 1639 | 1 US-08-334-698-5 | Sequence 5, Appl |
| 40 | 138.2 | 10.2 | 1639 | 1 US-08-228-932-5 | Sequence 5, Appl |
| 41 | 138.2 | 10.2 | 1639 | 1 US-08-468-939-5 | Sequence 5, Appl |
| 42 | 138.2 | 10.2 | 1639 | 2 US-08-406-855A-5 | Sequence 5, Appl |
| 43 | 138.2 | 10.2 | 1639 | 2 US-08-722-190-5 | Sequence 5, Appl |
| 44 | 138.2 | 10.2 | 1639 | 3 US-08-244-354-5 | Sequence 5, Appl |
| 45 | 138.2 | 10.2 | 1639 | 3 US-09-206-899-5 | Sequence 5, Appl |

ALIGNMENTS

RESULT 1
US-09-016-434-1181
; Sequence 1181, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 37,071
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; TELEPHONE/DOCKET NUMBER: PA-0002 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9178197
; US-09-016-434-1181
Query Match 99.8%; Score 1349.8; DB 4; Length 2072;
Best Local Similarity 99.9%; Pred. No. 1.6e-252;

Matches 1351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGACCAACAGAGACCCCTTACCTGCTGAGAGGCAAGCGGCACTAGCGGCGCATCAC 60
 DB 413 ATGAGACCAACAGAGACCCCTTACCTGCTGAGAGGCAAGCGGCACTAGCGGCGCATCAC 472
 QY 61 TTCTCTATCTCTTATCACTTTCGGAACGCTGTGATCTTCGCTGTGATGACAC 120
 DB 473 TTCTCTATCTCTTATCACTTTCGGAACGCTGTGATCTTCGCTGTGATGACAC 532
 QY 121 CGCTGCTGCGGCGGCTTCAAGAACCTGTCTGTGCTGTGCTGCGCGCGGACATCTG 180
 DB 533 CGCTGCTGCGGCGGCTTCAAGAACCTGTCTGTGCTGTGCTGCGCGCGGACATCTG 552
 QY 181 GTGCGAGGCTCATCATCTCTTCTGCTGCGCAAGAGCTGTGAGGCTACTGTACTTC 240
 DB 593 GTGCGAGGCTCATCATCTCTTCTGCTGCGCAAGAGCTGTGAGGCTACTGTACTTC 652
 QY 241 CGGCGACGTGAGTGCAGAGTGTACCTGCGCTGAGCGCTCTTCTGCACTTCGTCATC 300
 DB 653 CGGCGACGTGAGTGCAGAGTGTACCTGCGCTGAGCGCTCTTCTGCACTTCGTCATC 712
 QY 301 GTGCACTGTGCGCATGAGCTGAGACCTGTAAGCGGCGGCGGCTGAGTAC 360
 DB 713 GTGCACTGTGCGCATGAGCTGAGACCTGTAAGCGGCGGCGGCTGAGTAC 772
 QY 361 AACTCCAGGCGACCCCGGCGCGCATCAAGTGCATCATCTGTGTGCTCATCGCC 420
 DB 773 AACTCCAGGCGACCCCGGCGCGCATCAAGTGCATCATCTGTGTGCTCATCGCC 832
 QY 421 GCGCTCATCTGCTGCGGCGGCTCATCTCAAGGCGGCAAGAGGCGGCGGCGGCGG 480
 DB 833 GCGCTCATCTGCTGCGGCGGCTCATCTCAAGGCGGCAAGAGGCGGCGGCGGCGG 922
 QY 481 CGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
 DB 893 CGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 952
 QY 541 TTCTTGTCTCTTCTCTCTCATATGATCTGTGCACTGCGGCACTTCTGATGCGCAA 600
 DB 953 TTCTTGTCTCTTCTCTCTCATATGATCTGTGCACTGCGGCACTTCTGATGCGCAA 1012
 QY 601 CGGAGAACCGGAGAGGTCCAGGCGCAAGGCGGCGGCGGCGGCGGCGGCGGCGG 660
 DB 1013 CGGAGAACCGGAGAGGTCCAGGCGCAAGGCGGCGGCGGCGGCGGCGGCGGCGG 1072
 QY 661 CGGCGACCGGACGATGCTGCGGCTTGTGCGCTCAAGCACTGCGGCGGCGGCGG 720
 DB 1073 CGGCGACCGGACGATGCTGCGGCTTGTGCGCTCAAGCACTGCGGCGGCGGCGG 1132
 QY 721 GCTTCTGCGAGAGGTCAACGCACTGCAAGTCTCACTGCGGCGGCGGCGGCGGCGG 780
 DB 1133 GCTTCTGCGAGAGGTCAACGCACTGCAAGTCTCACTGCGGCGGCGGCGGCGGCGG 1192
 QY 781 ACCCTGAAGATATCTGAGAGCCCGGCGCTTTCGCAAGTGTGCGGCGGCGGCGG 840
 DB 1193 ACCCTGAAGATATCTGAGAGCCCGGCGCTTTCGCAAGTGTGCGGCGGCGGCGG 1252
 QY 841 GCGCGAGGCGGAGAGAGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 900
 DB 1253 GCGCGAGGCGGAGAGAGAGGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1312
 QY 901 GAGAGAGAGAGAGAGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 960
 DB 1313 GAGAGAGAGAGAGAGAGAGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 1372
 QY 961 TGAGCTTGAAGCGGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 1373 TGAGCTTGAAGCGGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1432
 QY 1021 GCGCGAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 DB 1433 GCGCGAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1492

QY 1081 GCGAGGTGACCCCGGAGAGAGCGCTTCACTTGTGCTGCTGCTGCTGCTGCTT 1140
 DB 1493 GCGAGGTGACCCCGGAGAGAGCGCTTCACTTGTGCTGCTGCTGCTGCTGCTT 1552
 QY 1141 GTGCTGTGCTGCTTCCCTTCTTCTGAGTCAAGCTGCGGCGGCGGCGGCGGAGC 1200
 DB 1553 GTGCTGTGCTGCTTCCCTTCTTCTGAGTCAAGCTGCGGCGGCGGCGGCGGAGC 1612
 QY 1201 TCGAAGTGCCTCATGCTGCTTCTTCAAGTCTTCTGAGTCAAGCTGCGGAGTCA 1260
 DB 1613 TCGAAGTGCCTCATGCTGCTTCTTCAAGTCTTCTGAGTCAAGCTGCGGAGTCA 1672
 QY 1261 CTGAAGCTGCTTATCTAAGCACTTCAAGCACTTCAAGCACTTCAAGCACTTCA 1320
 DB 1673 CTGAAGCTGCTTATCTAAGCACTTCAAGCACTTCAAGCACTTCAAGCACTTCA 1732
 QY 1321 CTGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353
 DB 1733 CTGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1765

RESULT 2
 US-09-016-434-1256
 ; Sequence 1256, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Jeffrey A. Young
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1256:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1382 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: g219405
 ; US-09-016-434-1256
 ;
 ; Query Match 32.8%; Score 444; DB 4; Length 1382;
 ; Best Local Similarity 62.2%; Pred. No. 1.7e-77;
 ; Matches 823; Conservative 0; Mismatches 405; Indels 96; Gaps 4;

QY 13 GACCCCTACCTGCGTGAAGCCACAGCGCCATAGCCGCGGCATCATCTTCTCATCTTC 72
 DB 132 GGCAGACTCTGCG 191
 QY 73 TTTTACCATTTTGGGCAAGCTCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
 DB 192 TTACCGTGTGTGGGCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
 QY 133 GCGCCCTACAGACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192
 DB 252 GCGCCACAGACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
 QY 193 ATCATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252
 DB 312 GTCATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
 QY 253 TCCGAGGTGTACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
 DB 372 TCCGCGCTGTACCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
 QY 313 GGCATCAGCTGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 372
 DB 432 GGCATCAGCTGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
 QY 373 ACCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
 DB 492 ACACACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
 QY 433 CTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 492
 DB 552 TTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
 QY 493 AAGCTCAACAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
 DB 609 GGCCTCAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
 QY 553 TGCCTCATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
 DB 669 TGCCTCATCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
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 DB 822 GGGCACTGCG 881
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 DB 903 TTGCG 962
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 DB 963 CAGGAG 1022
 QY 973 CCGCGCGCT 1032
 DB 1023 CTGTGCG 1082
 QY 1033 CTGGGAG 1092
 DB 1083 AGCAGC-----GTGTGCG 1115

QY 1093 CGGAG 1152
 DB 1116 CCGAG 1175
 QY 1153 TTCCCTCTTCTTCAAGCTGAG 1212
 DB 1176 TTCCCTCTTCTTCAAGCTGAG 1235
 QY 1213 CATGGCTCTTCAAGCTGAG 1272
 DB 1236 GCGCGCGCTTCAAGCTGAG 1295
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 DB 1296 ATCTACAGGTCTTCAAG 1355
 QY 1333 TCGA 1336
 DB 1356 AGCA 1359
 RESULT 3
 US-09-016-434-1180
 ; Sequence 1180, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1180:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3604 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: 9178195
 US-09-016-434-1180
 Query Match 31.8%; Score 430; DB 4; Length 3604;
 Best Local Similarity 61.7%; Pred. No. 9.9e-75;
 Matches 832; Conservative 0; Mismatches 435; Indels 81; Gaps 6;


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Db      671 TCATTATCGTGTGACACATCATCGGGAACATCTGATGTTCTGAGTGTTCACCTACA 730
Oy      122 GCTGCTGCGCCGCCCTCAGAACTGTTCCTGGTGTGCTGGCCGCCGCCGACATCTGG 181
Db      721 AGCCCTGTGCGATCTGTCCAGAACTTCTTCATAGTTTCGCTGGCGGTCGACATCCACA 790
Oy      182 TGGCAGCGCTCATCATCCCTTCTGCGCTGGCCACGAGCTGTGGGGCTTACCTGGTACTTCC 241
Db      791 TGGCCCTTCTGTGTCTGCGCTTTCACAGTGGCTTACTTCATCTCGAGCGCGCTGGAGTTGC 850
Oy      242 GGCAGCAGTGTGTGCGAGGTGTACTGTGGCGCTCGAGTGTCTTCTTGTGACCTGTCCATTCG 301
Db      851 GCATCACACTGTGTGCAAGCTGTGTGGCTCACCTGTGAGGTGTGTGTGTGTGCACTACTCATTC 910
Oy      302 TGCACCTGTGTGCGCCATCAAGCTTGAACCGCTACTGGCGCGTGAAGCGCGCTGAGATACA 361
Db      911 TGAACCTGTGTGTCCATAGCCCTCGACCGGTACTGGGGCCATTCAGAACCCCATCACTAATG 970
Oy      362 ACTCCAAACGCAACCCCGCGCGGCATCAAGTGCATATCTCACTGTGTGGCTTACATGCGCG 421
Db      971 CCGAAGAAAGAGACCGTTGGTGTGGCTCTGTCTCTTATCTCCGGGGTGTGTGCTACTTTCGC 1030
Oy      422 CCGTATCTCTGCTGTGCGCCCTCATCTCAAGAGGCAACGAGGGCCGCCAGCGCGCGGCG 481
Db      1031 TGCTGATTAAGTGTGTCCGCCCTTGTATGTGCTGAGACAGTGTGCGGACGATTCACAAGG 1090
Oy      482 GCGCCAGTGCAGAGCTCAACGAGAGGCGCTGTATACCTGTGCTTCCAGCATCGATCTT 541
Db      1091 CCAAGCCCTGTGAGCTGTACCTGTGACGCAAGGCTTAGTGATCTTACTCTTGTGCGTGGCTCT 1150
Oy      542 TCTTGTCTCTTGTGCTCTCATCATGATCTTGTGTACTCTGCGGATCTTACGTGATGCGCAAC 601
Db      1151 TCTTTATTTCTCGTGTGCAATCAAGAGATGTCTTACATGAGATCTTGTGTGTGCGACGCGC 1210
Oy      602 GCAGCAACGCGAGAGGTCCCGAGGGCCAA 629
Db      1211 GCGGCTTAAGGAGCGAGCCAGCGGCCAA 1238

RESULT 5
US-08-194-338-1
: Sequence 1, Application US/08194338
: Patent No. 5474898
: GENERAL INFORMATION:
:   APPLICANT: Venter, John C.
:   APPLICANT: Fraser, Claire M.
:   APPLICANT: McCombie, William R.
:   TITLE OF INVENTION: OCTOPAMINE RECEPTOR
:   NUMBER OF SEQUENCES: 16
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Knobbie, Martens, Olson and Bear
:   STREET: 620 Newport Center Drive, Sixteenth Floor
:   CITY: Newport Beach
:   STATE: CA
:   COUNTRY: USA
:   ZIP: 92660
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   OPERATING SYSTEM: IBM PC compatible
:   SOFTWARE: Patentin Release #1.0, Version #1.25
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08-194,338
:   FILING DATE: 08-FEB-1994
:   CLASSIFICATION: 435
:   PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US 07/676,174
:   FILING DATE: 28-MAR-1991
:   ATTORNEY/AGENT INFORMATION:
:   NAME: Israelien, Ned A.
:   REGISTRATION NUMBER: 29,655
:   REFERENCE/DOCKET NUMBER: NH101.001DV1
: TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 319..2124
US-08-194-338-1

Query Match      12.1%; Score 163.4; DB 1; Length 3335;
Best Local Similarity 55.8%; Pred. No. 3.3e-23;
Matches 351; Conservative 0; Mismatches 276; Indels 2; Gaps 2;

QY      2 TGAACCAAGGAGAACCCCTTACTCGGTGCAGGAGCAGAGGGGCCATGACGGGCGCATCACT 61
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QY      62 TCCTCATTTCTCTTAACCATCTTGCGCAAGCTCTGTGTATCTCTGGCTGTGTAAACACC 121
DB      671 TCATTATGTGTCTGACCAATCATCGGGAACATCTGTGTATCTTAAGTGTTCACCTACA 730
QY      122 GCTGCTGCGGGGCCCTCAGAAACGTGTTCCGTGTTGCTGCGCGCGCGCGAGATCTCTGG 181
DB      731 AGCGCTGCGGATGCTCCAGAACTTCTTCATAGTTTGCTGTGCGGTGCGGATCTCACGG 790
QY      182 TGGCAGCGCTCATCATCCCTTTCTCGCTGCGCAACGAGCTGCTGGGCTCATGTACTTCC 241
DB      791 TGGCCCTTCTGTGTGTGCTGCTTCAACGTCGCTTACTGTGATCTGCGGGGCGTGGAGTTCC 850
QY      242 GCGCAGCGGTGTGCGAGGTATCTGTGCGCTGCAAGTGTCTTTTGCACTCTGTTCATCG 301
DB      851 GCATTCACCTGTGCAAGCTGTGTGTCTCACTGCGAAGTGTGTGTGCACTAAGCTTCATCC 910
QY      302 TGCA-CCTGTGCGGCATCAGCCTGTGACCGGCTGAGCGGCGGTGAGCGCGCTGGAGTAC 360
DB      911 TGAACCTGTGTGCTATGCTTCCCTGACCGGTACTGTGGGCATTTA-CGAGCCATCACTAT 969
QY      361 AACTTCAGGCGCAACCCCGCGCGCATCAAGTCAATCTCACTGTGTGCTCATGCC 420
DB      970 GCCAGAAGAGAGACCGTTGTGTGTGTGTCTGTCTCTCATCTCCGGGGTGTGTACTTTGG 1029
QY      421 GCGGTGATCTGTGCTGCGGCCCTTACTATCAAGGGCGAACAAGGCCCCCAGCGCGCGG 480
DB      1030 CTGCTGATTAATAAGTATCGCGCGTGTATGCGGTGGAACAACAAGTTCACAAGC 1089
QY      481 CGCCCCAAGTTCAGCTCAACAGAGAGGCGCTGTATCACTCGGCGCTCAGATGGATCT 540
DB      1090 GCGACGCGCTGTGAGCTGAGCTCTGACAGAGAGGCTAAGTACTACTCTGCTGTGGCTCC 1149
QY      541 TTCTTTTGCTCTGTGCTCATCATGATCTTGTCTACCTGCGGCTCACTGATGAGCCAAA 600
DB      1150 TTCCTTATTTCCGTGCGGCATATGACATGCTGTCTAATCGAGATCTTGTGTGCAACGGG 1209
QY      601 CGCAGCAACGCGCAGAGGTGCCAGGGGCCAA 629
DB      1210 CGCGGCTTAAGGAGCGAGCGAGGGCCAA 1238

RESULT 6
US-08-722-001-17
; Sequence 17, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
```

APPLICANT: Lee, Hee-Yoon
APPLICANT: Bell, Ian M.
TITLE OF INVENTION: ALPHALIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-17

Query Match 11.7%; Score 158.6; DB 1; Length 921;
Best Local Similarity 57.0%; Pred. No. 2.4e-22;
Matches 312; Conservative 0; Mismatches 229; Indels 6; Gaps 1;

63 CCTCATCTCTTTTACCATCTTGGCAACGCTGCTGATCTGCTGTGTGACACCG 122
170 CTTTATCTCTTTGGCATCTGAGGCAACATCTAGTATCTTGTCTGTGGCTGGCAACCG 229
123 CTCGCTGGCGCCCTCAGAACCTGTTCTGTGCTGCGCGCGCGCATCTGTGT 182
230 GCACCTGGAGAGCGCCACCACTATTGTCAACTGSCCATATGGCCGACCTGT 289
183 GGCCACGCTCATCATCTCTTCTGCTGCTGCAAGAGCTGTGGGCTAAGTGAATTCCG 242
290 GAGCTTACCGCTTCCGCTTCTAGCGGCGCTAGAGGTGCTCGGCTAAGTGGTGGG 349
243 GCGCAGCTGTGGCGAGGTGTACTGTGGCTGAGCGTGTCTTCTTGGCACTGTGCTCATCT 302
350 GCGGATCTTCTGTGACATCTGGGCAAGCGGTGATGTCTGTGCTGCAAGAGGTTCATCTT 409
303 GCACCTGTGGCGCATCTGAGCGCTGCACTGAGCGCGTGAAGCGCGCTGAGTCA 362
410 GAGCTGTGGCGCATCTTCTGATCGTCACTGAGGAGTGGCTAAGTCTCTGCAAGTATCC 469
363 CTCGACGCGCACCCCGCGCGCGCATCAAGTCAATCTCACTGTGTGGCTCATGCGCCG 422
470 CACGCTGTGATCACCGGAGAGAGGCGCATCTTGGCGCTGCTCAAGTGTCTGTGTCCAC 529
423 CGTCAATCTGTGCGCGCCCTTCTATCTCAAGAGGCGACAGAGGCGCGCGCGGCGG 482
530 CGTCAATCTGTGCGCGCCCTTCTGTGGTGAAGAGCGCGGCAACCA-----GATGA 583

483 CCCCAGTGAAGTCAACAGAGGCTGTGATCTTGGCCCTCGACATCGATCTTT 542
584 CAGAGATGGGGGTGACCGAAGAACCTTCTATGCGCTTCTCTCTCTGAGCTCTT 643
543 CTTTGTCTTGGCTTCAATGATCTTGTCTACCTGGCATCTTACTGATCCGCAACG 602
644 CTACATCCCTCTGCGGCTTATCTGATGATCTGCGGCTGTATATGATGGCAAG 703
603 CAGCAAC 609
704 AACCAAC 710

RESULT 7
US-08-722-001-24
Sequence 24, Application US/08722001
Patent No. 5760054
GENERAL INFORMATION:
APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Nerenberg, Jennie B.
APPLICANT: Lee, Hee-Yoon
TITLE OF INVENTION: ALPHALIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-24

Query Match 11.7%; Score 158.6; DB 1; Length 1567;
Best Local Similarity 57.0%; Pred. No. 2.5e-22;
Matches 312; Conservative 0; Mismatches 229; Indels 6; Gaps 1;

63 CCTCATCTCTTTTACCATCTTGGCAACGCTGCTGATCTGCTGTGTGACACCG 122
170 CTTTATCTCTTTGGCATCTGAGGCAACATCTAGTATCTTGTCTGTGGCTGGCAACCG 229
123 CTCGCTGGCGCCCTCAGAACCTGTTCTGTGCTGCGCGCGCATCTGTGT 182

| | | | |
|----|-----|--|-----|
| Db | 220 | GCACCTGGCGAAGGCCAACCACTACTTCAATGTGCAACCTGGCCATAGCCGACCTGCTGTT | 289 |
| Oy | 183 | GGCCACGCTCATCATCCCTTTTCTCGCTGGCCAAAGAGCTGAGGCTACTGTACTTTCCG | 242 |
| Db | 290 | GAGCTTACACCGTCTGCGCCCTTCTCAACGGGCCCTAGAGAGTGTCTGGCTTACGTGGGTGCTGGG | 349 |
| Oy | 243 | GGGCAAGAGTGTGAGGTGTACTGCTGGCGCTCAAGCGTGTCTTGTGCAACCTGTGCAATCGT | 302 |
| Db | 350 | GGGAGCTTCTGTGATCTGTGGGACACCGGAGATGTCTGTGTGCAACAGCGTCAATCTT | 409 |
| Oy | 303 | GCACTGTGTGCGGCATCAGCCTGTGACCGCTTAACTTGAGCGCGGCGCTGTGAGTACA | 352 |
| Db | 410 | GAGCCTGTGTGGCGCATCTTCATGTGATCGATCGGGGTGGCGCTACTCTTGTGAGATGCC | 469 |
| Oy | 353 | CTCCAAAGCGCACCCCGCGCGCGCATCAAGTGATCATCTTCACTGTGTGCTCATTCGCCGC | 422 |
| Db | 470 | CACGCTGTGTCAACCGGAGGAAAGGCCATCTTGGCGCTGCTAGTGTGTGGGTCTTGTTCAC | 529 |
| Oy | 423 | CGTATATTCGCTGCGCGCCGCTCATCTCAAGAGGCGACAGAGGCCCCCAGCGCGCGGGCG | 482 |
| Db | 530 | CGTATATCTCAATCGGGCGCTCTCTTGGGTGGAAAGAGCGGCCAACCCAA-----CGATGA | 583 |
| Oy | 483 | CCCCCAGTGCAAGCTCAACAGAGAGGCGTGTATCATCTGTGACCTTCCAGCATCGGATCTTT | 542 |
| Db | 584 | CAGGAGTGTGGGGGTACCGGAAGAACCTTCTATGTGCCCTTCTTCTCTTGTGGGCTCTT | 643 |
| Oy | 543 | CTTTGCTCTGTGCGCTCATCATGATCTTGTGTCTACCTGCGCATCTTACCTGATGCCAAAG | 602 |
| Db | 644 | CTACATCTCTGTGGCGGTCTATCTTAATCATGTACTCGGTGTCTATATATAGTGCACAAAG | 703 |
| Oy | 603 | CAGCAAC 609 | |
| Db | 704 | AACCAAC 710 | |

RESULT 8
 US-08-334-698-3
 Sequence 3, Application US/08334698
 Patent No. 5556753
 GENERAL INFORMATION:
 APPLICANT: Jonathan A. Bard et al.
 TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
 TITLE OF INVENTION: Receptors and Uses Thereof
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DUNHAM
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/334,698
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/952,798
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 376901
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: (212) 422523 COOP UI
 INFORMATION FOR SEQ ID NO: 3:

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SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-334-698-3

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US RESULT 9
US-08-228-932-3
Sequence 3, Application US/08228932
Patent No. 5578611
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chin,
 Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
 PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York

| | | | |
|----|-----|---|-----|
| Oy | 303 | GCACCTGTGCGCATCAGCCTGGACCGCTACTGAGCGCGTGAAGTACAA | 362 |
| Db | 525 | GAGCTGTGCGCATTCATGATGATGCTACATCGGAGGTGCGTTACTCTTGGACGATTC | 584 |
| Oy | 363 | CTCCAAAGCGCACCCGCGCGCGCATCAAGTGCATCTTCATCTGTGTGCTCATCGCCG | 422 |
| Db | 585 | CACGCTGGTCAACCCGAGGAGAGGCCATCTTTGGCGCTGTACGTGTCTGGGTCTTGTTCAC | 644 |
| Oy | 423 | CGTCATCTTGCGCTGCGGCCCTTCATTTACAAGGGCGACAGAGGCCCCCAAGCGCGCGGCG | 482 |
| Db | 645 | CGTCATCTTCATCGGGCCCTCTCCTTGGTGGAAAGAGCGCGCACCCAA-----CGATGA | 698 |
| Oy | 483 | CCCCAGTGCAGAGCTCAACACAGAGGCCCTGTGATCATCTGTGAGCTCCAGCATCGGATCTTT | 542 |
| Db | 699 | CAGGAGATGCGGGGGTCAACGGAAGAACCTTTTATATGCGCTTCTCTCTCTGAGGCTCTCTT | 758 |
| Oy | 543 | CTTTGCTCCTTGCGCTCATCATGATCCTTGTCTAACCGCGCATTAACCTGATCGCCAAAG | 602 |
| Db | 759 | CTACATCCCTCTGGCGGTCATTTCTAGTCATGTACTCGCGTCTTATATAGTGGCCAAAG | 818 |
| Oy | 603 | CAGCAAC | 609 |
| Db | 819 | AACCAAC | 825 |

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11 RESULT
12 US-08-406-855A-3
13 Sequence 3, Application US/08406855A
14 Patent No. 5861309
15 GENERAL INFORMATION:
16 APPLICANT: Jonathan A. Bard et al.
17 TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
18 TITLE OF INVENTION: Receptors and Uses Thereof
19 NUMBER OF SEQUENCES: 23
20 CORRESPONDENCE ADDRESS:
21 ADDRESSEE: Cooper & Dunham LLP
22 STREET: 1185 Avenue of the Americas
23 CITY: New York
24 STATE: New York
25 COUNTRY: U.S.A.
26 ZIP: 10036
27 COMPUTER READABLE FORM:
28 MEDIUM TYPE: Floppy disk
29 COMPUTER: IBM PC compatible
30 OPERATING SYSTEM: PC-DOS/MS-DOS
31 SOFTWARE: PatentIn Release #1.30
32 CURRENT APPLICATION DATA:
33 APPLICATION NUMBER: US/08/406,855A
34 FILING DATE: 21-AUG-1995
35 CLASSIFICATION: 435
36 ATTORNEY/AGENT INFORMATION:
37 NAME: White, John P.
38 REGISTRATION NUMBER: 28,678
39 REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KOB
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: (212) 278-0400
42 TELEFAX: (212) 391-0526
43 INFORMATION FOR SEQ ID NO: 3:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 1738 base pairs
46 TYPE: nucleic acid
47 STRANDEDNESS: single
48 TOPOLOGY: unknown
49 MOLECULE TYPE: DNA (genomic)
50 HYPOTHETICAL: N
51 ANTI-SENSE: N
52 FEATURE:
53 NAME/KEY: CDS
54 LOCATION: 124..1663
55 OTHER INFORMATION:
56 US-08-406-855A-3

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Query Match      11.6%: Score 157; DB 2; Length 1738;
Best Local Similarity 56.9%: Pred. No. 5.2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

OY CCTGATTTCTTTTACCATCTTCGCGAACGCTCTGATCATCTCGCTGTGTGACGACGCG 122
DB CTTATCTCTCTTTGGCATCGTGGGCAACATCTTAGTATCTTGTCTGTGGCTCGAACG 344
OY 123 CTCGTGCGCGCCCTTCAGAACCTGTTCTGTGTCTGCTGCGCGCGCGCAATCTGTGT 182
DB 345 GCACCTGTGGAGCGGCCAACCACTATTGTGAACCTGTGCATGTGGCGCACTGTGTT 404
OY 183 GGGCAGCGTATCATATCCCTTTCTGTGCTGGGCCAAGAGCTGTGGGCTATCTGTACTTCCG 242
DB 405 GAGCTTACCGCTCTGCTCTTCTAAGCGGCGCTTAGAGGTGTCTGGCTAATGTGGTGTGG 464
OY 243 GCGCAGCTGTGTGCGAGGTGTACTGTGGCGCTCGACGTGCTTTGTGCACTTGTCCATCGT 302
DB 465 GCGGATCTTCTGTGTACATCTGTGGGAGCGCGTGTGATGTCTGTGTCTGTGCAAGGCTCCATCT 524
OY 303 GCACCTGTGCGCATCAAGCTGTGACCGCTACTGTGGCGGTGAGCGCGCGCTGTGAGTACAA 362
DB 525 GAGCTGTGCGCATCTTCATCATGTGCTAATGTGGGTCGCTAATCTTCTGTGCAGTATCC 584
OY 363 CTCCAGCGGCAACCGCGCGCGCATCAAGTGTATCTCTCATGTGTGGCTCATATCGCCG 422
DB 585 CAGCTGTGTACCCGAGGAAAGGCGATCTTGGCGCTGTCTAGTGTGTGGGCTTGTGTAC 644
OY 423 CGTATCTCTGCTGCGCGCCCTCATCTCAAGGGGCGACCGAGGCGCCCGACGCGCGGCG 482
DB 645 CGTATCTTCATCGGGGCTCTCTCTTGGGTGAAAGAGCGGCACTCCAA-----CGATGA 698
OY 483 CCCCCAGTGAAGCTCAACGAGAGGCTGTGTACATCTGTGACTCGACATCGGATCTTT 542
DB 699 CAGGAGTGGGGGTCAACGAAAGACCTTGTATGCCCTTCTCTCTGTGGGCTCCTT 758
OY 543 CTTTGTCTCTTCTGCTCATGTATCTTGTGTACTGTGGCATCTAACCTGATCGCGCAACG 602
DB 759 CTATACCTCTCTGTGGGCTCATCTGTATGTACTGTGCGGTGTCTATATAGTGGCGAAG 818
OY 603 CAGCAAC 609
DB 819 AACCAAC 825

RESULT 12
US-08-722-190-3
; Sequence 3, Application US/08722190
; Patent No. 5990128
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George
; APPLICANT: Chiu, Theresa A. Branchek, John M. Metzger and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTRATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,190
; FILING DATE: 4-APR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.

```

REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-722-190-3

Query Match 11.6%; Score 157; DB 2; Length 1738;
Best Local Similarity 56.9%; Pred. No. 5.2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

63 CCTATTCTTTTACATCTTGGCAAGCTCTGATCTCTGCTGTGTAACAGCG 122
285 CTTATCTCTTTGGCATCTGAGCAATCTAGTATCTGTCTGAGCGCAACCG 344
123 CTGCTGGGCGCCCTGAGACCTGTCCTGCTGCTGCGCCCGGCAATCTGAT 182
345 GCACCTGGAGAGCGCCCAACCACTTATGTAACCTGAGCCGACCTGCTGTT 404
183 GAGCAAGCTCATCTCTTCTGCTGAGCAAGCTGAGGCTGAGTACTGCTCG 242
405 GAGCTTACAGCTCTGCTGCTGAGGAGCTGAGTCTGCTGCAAGCGTCACTCT 464
243 GCGAAGCTGAGGAGGAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 302
465 GCGAATCTTCTGATCACTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 524
303 GCACTGTGCGCCATCAAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 362
525 GAGCTGTGCGCCATCAAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 584
363 CTCAAGCGAGCGCCCGGCGCATCAAGCTGATCTCTGCTGAGGCTGAGGCG 422
585 CAGCTGTGAGCGCGGAGAGGAGCACTGAGGCTGAGGCTGAGGCTGAGGCT 644
423 CGTATCTGCTGCGCCCTGATCAAGAGGAGCGAGGCGCCGAGCGCGGCGG 482
645 CGTATCTGATCGGCGCTCTCTTGGGAGAGAGGAGCGGAGCGCA-----CGATGA 698
483 CCCCCAGTGAAGCTCAAGAGAGGCTGATCACTGAGGCTGAGGCTGAGGCTG 542
699 CAGAGAGTGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 758
543 CTTGCTGCTGCTGATCAATGATCTTGTCTTACTGAGGAGTCACTGAGGAG 602
759 CTACATCTCTGAGGAGGAGTATGATCACTGAGGAGTATGAGGAGGAG 818
603 CAGCAAC 609
819 AACCAAC 825

RESULT 13
US-08-244-354-3
Sequence 3, Application US/08244354
Patent No. 6015819
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO

TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,354
FILING DATE: April 1, 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-244-354-3

Query Match 11.6%; Score 157; DB 3; Length 1738;
Best Local Similarity 56.9%; Pred. No. 5.2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

63 CCTATTCTTTTACATCTTGGCAAGCTCTGATCTCTGCTGTGTAACAGCG 122
285 CTTATCTCTTTGGCATCTGAGCAATCTAGTATCTGTCTGAGCGCAACCG 344
123 CTGCTGGGCGCCCTGAGACCTGTCCTGCTGCTGCGCCCGGCAATCTGAT 182
345 GCACCTGGAGAGCGCCCAACCACTTATGTAACCTGAGCCGACCTGCTGTT 404
183 GAGCAAGCTCATCTCTTCTGCTGAGCAAGCTGAGGCTGAGTACTGCTCG 242
405 GAGCTTACAGCTCTGCTGCTGAGGAGCTGAGTCTGCTGCAAGCGTCACTCT 464
243 GCGAAGCTGAGGAGGAGTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 302
465 GCGAATCTTCTGATCACTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCT 524
303 GCACTGTGCGCCATCAAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 362
525 GAGCTGTGCGCCATCAAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 584
363 CTCAAGCGAGCGCCCGGCGCATCAAGCTGATCTCTGCTGAGGCTGAGGCG 422
585 CAGCTGTGAGCGCGGAGAGGAGCACTGAGGCTGAGGCTGAGGCTGAGGCT 644
423 CGTATCTGCTGCGCCCTGATCAAGAGGAGCGAGGCGCCGAGCGCGGCGG 482
645 CGTATCTGATCGGCGCTCTCTTGGGAGAGAGGAGCGGAGCGGAGCGCA-----CGATGA 698

QY 483 CCCCCAGTCAAGCTCAACGAGGCGCTGGTACATCTGGCCTCCAGCATGGATCTTT 542
| | | | |
DB 699 CAGAGGTGCGGGGTCAACGAGAACCTTCTATGCCCTCTCTCTGGGCTCCTT 758
| | | | |
QY 543 CTTTGCTCTTGCTGCTATCATGATCTTGTCTTACCTGGCATCTACTATGCCAAG 602
| | | | |
DB 759 CTACATCCCTTGGCGGCTATCTAGTCACTGCGGTCTATATATGTGGCAAG 818
| | | | |
QY 603 CAGCAAC 609
| | | | |
DB 819 AACCAAC 825
| | | | |
RESULT 14
US-09-206-899-3
; Sequence 3, Application US/09206899
; Patent No. 6083705
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,899
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,855
; FILING DATE: 21-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1683
; OTHER INFORMATION:
; US-09-206-899-3
Query Match 11.6%; Score 157; DB 3; Length 1738;
Best Local Similarity 56.9%; Pred. No. 5, 2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;
QY 63 CCGCATCTCTTACCATCTTGGCAAGCTCTGGTCACTCTGGCTGTGTTACGACCG 122
| | | | |
DB 285 CTTGATCCCTCTTGGCATCTGGGCAACATCTTATGTCATCTTGTGTGGCTGCAACG 344
| | | | |
QY 123 CTCGTCGCGCGCCCTCAGAACCTGTCTGCTGTGCTGGCGCGCGCAACATCTGTG 182
| | | | |

DB 345 GCACTGCGGAGACCCCAACCACTACTTCACTTGTCAACTGGCCAGCCGACCTGCT 404
| | | | |
QY 183 GGCACAGCTCATCATCCCTTTCTGCTGGCCCAACAGAGCTGTGGCTATGTAATCCG 242
| | | | |
DB 405 GAGCTTCAACCTCTGCTCCCTTTCTAGAGGCTCTTAAAGAGTCTGCTATCTGGGTG 464
| | | | |
QY 243 GCGCAGTGTGTGAGGTGTACCTGGCGCTGACGTCTCTTCTGACCTGTGCATGCT 302
| | | | |
DB 465 GCGGATCTTCTGTGACATCTGGGCAAGCGGTGATGTCGTGCTGACACGCTTCATCT 524
| | | | |
QY 303 GCACCTGTGGCCCATCATGCTGACCGCTACTCTGGCCCGGTGACCCGCTGTGATGCA 362
| | | | |
DB 525 GAGCTGTGGCCCATCTTCATCATGATCGATCAATCGGGGCGCTACTCTTCAATATCC 584
| | | | |
QY 363 CTCGAAGCGACCCCGCGCGCATCAAGTCAATCTCACTGTGTGCTATCGCCG 422
| | | | |
DB 585 CACGCTGTACCCCGGAGGAGGCAATCTTGGCGCTGTCACTGTGTGGTCTTGTCCAC 644
| | | | |
QY 423 CGTCAATCTGCTGCGCCCTCTCATCTACAGGCGCAACGAGCCCGCACCGCGCGG 482
| | | | |
DB 645 CGTCAATCTCATCGGCGCTCTCTTGGGTGGAAGAGCGCGCACCA-----CGATGA 698
| | | | |
QY 483 CCCCCAGTCAAGCTCAACGAGGCGCTGTACATCTTGGCTTCCAGCATGATCTTT 542
| | | | |
DB 699 CAGGAGTGGGGGTCAACGAGAACCTTCTATGCTCTCTCTCTCTGCGCTCTT 758
| | | | |
QY 543 CTTTGCTCTTGCTGCTATCATGATCTTGTCTTACCTGGCGCATCTCATGCGCAAG 602
| | | | |
DB 759 CTACATCCCTTGGCGGCTATCTAGTCACTGCGGTCTGTATATGTGGCAAG 818
| | | | |
QY 603 CAGCAAC 609
| | | | |
DB 819 AACCAAC 825
| | | | |

RESULT 15
US-09-444-783-3
; Sequence 3, Application US/09444783
; Patent No. 6420389
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, et al.
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,783
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-A-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFO: INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-09-444-783-3

Query Match 11.6%; Score 157; DB 4; Length 1738;
Best Local Similarity 56.9%; Pred. No. 5.2e-22;
Matches 311; Conservative 0; Mismatches 230; Indels 6; Gaps 1;

QY 63 CCTCATCTCTTTACCATCTTCCGCAACGCTTGGTCACTCTGCTGTGTGACCAACCG 122
DB 285 CTTTCATCTCTTTGCGCATCTGCGCAACATCTAGTCATCTTGTGTGCTGCAACCG 344
QY 123 CTGCTGCGCGCCCTCAGAACCTGTTCTGTGTGCTGCGCGCGCGCACTCTGCT 182
DB 345 GCACCTGCGGACCGCCCAACCACTTCACTTCACTGCGCACTGCGCGCACTGCTGT 404
QY 183 GGCACGCTCATCATCTCTTCTGCTGCGCAACGAGCTGCTGCGCTACTGTACTTCCG 242
DB 405 GAGCTTCACGCTCTGCGCTTCTCAGCGGCGCTAGAGTCTGCGCTACTGCGCTGCG 464
QY 243 GCGCACGTGTGAGAGGTGACCTGCGCTGCACTGCTCTTGTGCACTGCTGCACTGT 302
DB 465 GCGGATCTTCTGTGACATCTGCGCAACGCGGATGCTGTGCTGCAACGCTGCACT 524
QY 303 GCACCTGTGCGCGCATCAGCTTGAACGCTACTGCGCGCGCGCGCGCTGAGTACAA 362
DB 525 GAGCTGTGCGCATCTCCATCTGATCTGATCTGCGCGCGCTACTCTTGTGCACTATCC 584
QY 363 CTCGACGCGCACCGCGCGCGCATCAAGTCATCTCTCACTGTGTGCTCATGCGCGC 422
DB 585 CAGCTGTGTACCGCGGAGAAAGGCATCTGCGCGCTGCTCAGTGTCTGCGCTTGTCCAC 644
QY 423 CGTCATCTGCTGCGCGCGCTCATCTACAAAGGCGAGCAGAGGCGCGCGCGCGCG 482
DB 645 CGTCATCTGCTGCGCGCGCTCTCTTGTGTGAGAAAGAGACCGCGCACCA-----CGATGA 698
QY 483 CCCCAGTGAAGCTCAACGAGGAGGCTGTGATCATCTGCGCTTCCAGCATCGGATCTTT 542
DB 699 CAGGAGTGTGCGGCTCACCGAAGACCTTCTATGCGCTCTTCTCTCTGCGGCTCTTT 758
QY 543 CTTTGTCTCTGCTCATCTGATCTTGTCTTACCTGCGCATCTACTGATCGCCAAACG 602
DB 759 CTACATCTCTGCGGCTCATCTAGTCATGCTAGTCTATATAGTGTGCGCAAGAG 818
QY 603 CAGCAAC 609
DB 819 AACCAAC 825

Search completed: February 8, 2004, 01:28:47
Job time : 96.7987 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:38:27 / Search time 516.217 Seconds
(without alignments)
9654.769 Million cell updates/sec

Title: US-09-692-077D-1
Perfect score: 1353
Sequence: 1 atgagaccagcagacccta.....ggaccagagcgctgctga 1353

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA.*

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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|---------------|--------|----------------|--------|----|--------------------|--------------------|
| 1 | 1353 | 100.0 | 1353 | 15 | US-10-001-073-1 | Sequence 1, Appli |
| 2 | 1351.4 | 99.9 | 1353 | 9 | US-09-825-923-3 | Sequence 3, Appli |
| 3 | 1351.4 | 99.9 | 1353 | 15 | US-10-077-870-3 | Sequence 3, Appli |
| 4 | 1349.8 | 99.8 | 2072 | 12 | US-10-305-720-1181 | Sequence 1181, Ap |
| 5 | 1349.8 | 99.8 | 3274 | 15 | US-10-225-567A-41 | Sequence 41, Appli |
| 6 | 1325 | 97.9 | 1344 | 15 | US-10-001-073-2 | Sequence 2, Appli |
| 7 | 1323.4 | 97.8 | 1344 | 9 | US-09-825-923-1 | Sequence 1, Appli |
| 8 | 1323.4 | 97.8 | 1344 | 15 | US-10-077-870-1 | Sequence 1, Appli |
| 9 | 600.2 | 44.4 | 6904 | 13 | US-10-311-455-47 | Sequence 47, Appli |
| 10 | 512.6 | 37.9 | 6904 | 13 | US-10-311-455-47 | Sequence 47, Appli |
| 11 | 458.4 | 33.9 | 1386 | 15 | US-10-001-073-40 | Sequence 40, Appli |
| 12 | 448.8 | 33.2 | 1374 | 15 | US-10-001-073-42 | Sequence 42, Appli |
| 13 | 447.2 | 33.1 | 2826 | 15 | US-10-225-567A-43 | Sequence 43, Appli |
| 14 | 444 | 32.8 | 1382 | 12 | US-10-305-720-1256 | Sequence 1256, Ap |
| 15 | 444 | 32.8 | 1382 | 13 | US-10-101-510-754 | Sequence 754, App |

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| 16 | 443 | 32.7 | 1350 | 15 | US-10-001-073-25 | Sequence 25, Appli |
| 17 | 442.4 | 32.7 | 3653 | 15 | US-10-225-567A-39 | Sequence 39, Appli |
| 18 | 441.4 | 32.6 | 1350 | 15 | US-10-001-073-24 | Sequence 24, Appli |
| 19 | 430 | 31.8 | 3604 | 12 | US-10-305-720-1180 | Sequence 1180, Ap |
| 20 | 293.6 | 21.7 | 1758 | 13 | US-10-101-510-450 | Sequence 450, App |
| 21 | 262.6 | 19.4 | 7353 | 13 | US-10-311-455-46 | Sequence 45, Appli |
| 22 | 181.4 | 13.4 | 7353 | 13 | US-10-311-455-45 | Sequence 1402, Ap |
| 23 | 157 | 11.6 | 1738 | 12 | US-10-305-720-1402 | Sequence 3, Appli |
| 24 | 157 | 11.6 | 1738 | 15 | US-10-185-991-3 | Sequence 3, Appli |
| 25 | 157 | 11.6 | 1738 | 15 | US-10-238-129-3 | Sequence 3, Appli |
| 26 | 157 | 11.6 | 1738 | 15 | US-10-238-667-3 | Sequence 35, Appli |
| 27 | 157 | 11.6 | 1786 | 15 | US-10-225-567A-35 | Sequence 1172, Ap |
| 28 | 149.6 | 11.1 | 2002 | 12 | US-10-305-720-1172 | Sequence 33, Appli |
| 29 | 149.6 | 11.1 | 2130 | 15 | US-10-225-567A-33 | Sequence 1, Appli |
| 30 | 149.6 | 11.1 | 2140 | 15 | US-10-185-991-1 | Sequence 1, Appli |
| 31 | 149.6 | 11.1 | 2140 | 15 | US-10-238-129-1 | Sequence 1, Appli |
| 32 | 149.6 | 11.1 | 2140 | 15 | US-10-238-667-1 | Sequence 1, Appli |
| 33 | 147.6 | 10.9 | 1896 | 15 | US-10-270-333-83 | Sequence 83, Appli |
| 34 | 145.4 | 10.7 | 1704 | 15 | US-10-270-333-125 | Sequence 125, App |
| 35 | 143.4 | 10.6 | 463 | 11 | US-09-918-995-29557 | Sequence 29557, A |
| 36 | 142.6 | 10.5 | 2048 | 14 | US-10-052-589-1 | Sequence 1, Appli |
| 37 | 141 | 10.4 | 1548 | 15 | US-10-054-616A-8 | Sequence 8, Appli |
| 38 | 139.4 | 10.3 | 1548 | 15 | US-10-054-616A-9 | Sequence 9, Appli |
| 39 | 139.4 | 10.3 | 1548 | 15 | US-10-054-616A-11 | Sequence 11, Appli |
| 40 | 138.4 | 10.2 | 1098 | 13 | US-09-826-509-430 | Sequence 430, App |
| 41 | 138.4 | 10.2 | 1930 | 12 | US-10-305-720-1171 | Sequence 1171, Ap |
| 42 | 138.4 | 10.2 | 1930 | 15 | US-10-225-567A-7 | Sequence 7, Appli |
| 43 | 138.2 | 10.2 | 1639 | 15 | US-10-185-991-5 | Sequence 5, Appli |
| 44 | 138.2 | 10.2 | 1639 | 15 | US-10-238-129-5 | Sequence 5, Appli |
| 45 | 138.2 | 10.2 | 1639 | 15 | US-10-238-667-5 | Sequence 5, Appli |

ALIGNMENTS

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RESULT 1
US-10-001-073-1
; Sequence 1, Application US/10001073
; PUBLIC: INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-1
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| Query Match | 100.0% | Score 1353; | DB 15; | Length 1353; |
| Best Local Similarity | 100.0% | Pred. No. 0; | Mismatches 0; | Indels 0; |
| Matches 1353; | Conservative | 0; | Indels 0; | Gaps 0; |
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| DB | 1 | ATGAGCAACAGAGAGCCCTACTCTCGTGAGGAGCAGAGCGGACCATAGCGGAGCCATACCC | 60 | |
| QY | 61 | TTTCCTATTCTTTTACCACTCTTGGGCAACGCTCTGTCATCTCTGCTGTGTTACACAC | 120 | |
| DB | 61 | TTTCCTATTCTTTTACCACTCTTGGGCAACGCTCTGTCATCTCTGCTGTGTTACACAC | 120 | |
| QY | 121 | CGCTGCGGCGGCGCCCTCAGAACGCTTCTGCTGTCGTCGCGGCGGCGGACATCCCG | 180 | |
| DB | 121 | CGCTGCGGCGGCGCCCTCAGAACGCTTCTGCTGTCGTCGCGGCGGCGGACATCCCG | 180 | |
| QY | 181 | GTGGCAGCGCTCATATCCCTTTCTCGCTGAGCAAGAGCTGCGGCTACTGTAATTC | 240 | |
| DB | 181 | GTGGCAGCGCTCATATCCCTTTCTCGCTGAGCAAGAGCTGCGGCTACTGTAATTC | 240 | |

QY 241 CGGCGACGTGGTGGAGGTGTAACCTGAGCGCTCGACGTGCTTTCTGACCTGCTCATC 300
 DB 241 CGGCGACGTGGTGGAGGTGTAACCTGAGCGCTCGACGTGCTTTCTGACCTGCTCATC 300
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 US-09-825-923-3
 ; Sequence 3, Application US/09825923
 ; Patent No. US2001001638A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Snapir, Amir
 ; APPLICANT: Heinonen, Paula
 ; APPLICANT: Alhopuro, Pia
 ; APPLICANT: Karvonen, Matti
 ; APPLICANT: Koulu, Markku
 ; APPLICANT: Pesonen, Ulla-Mari
 ; APPLICANT: Scheinin, Mika
 ; APPLICANT: Salonen, Jukka T
 ; APPLICANT: Tuominen, Tomi-Pekka
 ; APPLICANT: Lakka, Timo A
 ; APPLICANT: Nyyssönen, Kristina
 ; APPLICANT: Salonen, Riitta
 ; APPLICANT: Kauphanen, Jussi
 ; APPLICANT: Valkonen, Veli-Pekka
 ; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
 ; FILE REFERENCE: Alpha-2B-AR variant
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: US/09/825,923
 ; PRIORITY FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1353
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1350)
 ; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
 ; OTHER INFORMATION: protein
 ; US-09-825-923-3
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 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 1 ATGACCAACAGAGACCCCTACTCGGTGACAGGCGCACAGGCGGCGCATGAGGCGGCGCATCAC 60
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 DB 61 TTCCTATCTCTTTACCACTTGTGGCAAGCTGTGATCATCTGAGTGTGACCAAGC 120
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 DB 181 GTGCGACGCTATCATCTTCTGCTGCGGCGCAAGAGCTGCTGAGTGTGCTGCTGCTGCTTTC 240
 QY 241 CGGCGGAGGTGTGCGAGTGTACTGTGCGCTGAGCGTGTGCTTGTGCACTGTGCTCATC 300
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[illegible]

RESULT 3
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:

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? APPLICANT: Salonen, Jukka T
? TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
? FILE REFERENCE: 0933-0183P
? CURRENT APPLICATION NUMBER: US/10/077,870
? CURRENT FILING DATE: 2002-05-21
? PRIOR APPLICATION NUMBER: FI 20010323
? PRIOR FILING DATE: 2001-02-20
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: Patentin Ver. 3.1
? SEQ ID NO 3
? LENGTH: 1353
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(1350)
? OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
? JS-10-077-870-3

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| Query Match | Score | DB | Length |
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| Matches 1352; Conservative | 99.9% | Pred. No. 0; | |
| | 0; | Mismatches 1; | Indels 0; Gaps 0; |

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| Db | 1 | ATGACACACAGGACCCCTTATCTCGGTGAGGCAACAGGGGCAATAGCGGCGCATACAC | 60 |
| Qy | 61 | TTCTCATTTCTTTTACCATCTTGCGGCAACGCTGTGATCTTGCTGTGTGACAGC | 120 |
| Db | 61 | TTCTCATTTCTTTTACCATCTTGCGGCAACGCTGTGATCTTGCTGTGTGACAGC | 120 |
| Qy | 121 | CGTGGCTGGGGGCCCCCTGAGAACCTGTTCCGTGGTGTGGCGGCGCCGCGCAATCTG | 180 |
| Db | 121 | CGTGGCTGGGGGCCCCCTGAGAACCTGTTCCGTGGTGTGGCGGCGCCGCGCAATCTG | 180 |
| Qy | 181 | GTGGCAGCGCTCATATCCCTTTCTCGGTGGCAACGAGCTGTGGCTACTGGTACTTC | 240 |
| Db | 181 | GTGGCAGCGCTCATATCCCTTTCTCGGTGGCAACGAGCTGTGGCTACTGGTACTTC | 240 |
| Qy | 241 | CGGCGCAGCTGGTGGAGGTGTACTCTGGCGCTCGAGCTCTTTCTGTGACCTGTGCATC | 300 |
| Db | 241 | CGGCGCAGCTGGTGGAGGTGTACTCTGGCGCTCGAGCTCTTTCTGTGACCTGTGCATC | 300 |
| Qy | 301 | GTGCACTGTGGGCATACGCTGGACGGCTACTGGGCGGTGAGCCGGCGGCTGGAGTAC | 360 |
| Db | 301 | GTGCACTGTGGGCATACGCTGGACGGCTACTGGGCGGTGAGCCGGCGGCTGGAGTAC | 360 |
| Qy | 361 | AATCCMAAGCAGCCCGCGCGCGCATCAAGTGATCATCTCACTGTGTGCTATCGCC | 420 |
| Db | 361 | AATCCMAAGCAGCCCGCGCGCGCATCAAGTGATCATCTCACTGTGTGCTATCGCC | 420 |
| Qy | 421 | GCGGTATCTCGCTGCGCGCTTATCTTACAAGGGCGACAGGGGCCCCAGCCGCGGGG | 480 |
| Db | 421 | GCGGTATCTCGCTGCGCGCTTATCTTACAAGGGCGACAGGGGCCCCAGCCGCGGGG | 480 |
| Qy | 481 | CGGCCCCAGTGAAGGTCAACAGGAGGCGTGTACATCCAGGCGTCAGCATGTGAACT | 540 |
| Db | 481 | CGGCCCCAGTGAAGGTCAACAGGAGGCGTGTACATCCAGGCGTCAGCATGTGAACT | 540 |
| Qy | 541 | TTCTTTGCTCTTTGCTCATCATGATCTTGTCTTACTGCGCATCTACCTGATGCCAAA | 600 |
| Db | 541 | TTCTTTGCTCTTTGCTCATCATGATCTTGTCTTACTGCGCATCTACCTGATGCCAAA | 600 |
| Qy | 601 | CGGAGAACCGGAGAGTCTCCAGGGGCAAGGGGGGGGCTGGGGCAGGGTGAATCCAAACAG | 660 |
| Db | 601 | CGGAGAACCGGAGAGTCTCCAGGGGCAAGGGGGGGGCTGGGGCAGGGTGAATCCAAACAG | 660 |
| Qy | 661 | CCCGGACCCGACCAATGATGGGGCTTTTGGCTCAGCGAAAATGCGACGCTTGAGCTCTGTG | 720 |
| Db | 661 | CCCGGACCCGACCAATGATGGGGCTTTTGGCTCAGCGAAAATGCGACGCTTGAGCTCTGTG | 720 |
| Qy | 721 | GCTTGTGCAGAGAGTCAACGACATCTGAAATCTCACTGGGGGAAGAGAGAGGGGAG | 780 |

Db 721 GCTTTCGACAGAGGTCAACGACACTCGAAGTCACTGGGGAGAAAGAGAGAGAG 780
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 QY 901 GAAG 960
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 QY 961 TCAGCTTGACAGCCCGGCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
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 QY 1021 GGGCAGGTGCTCCCTGGGACAGGGGCTGGGCTGTAAGTGGGCAAGTGGGCTGAGAG 1080
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 QY 1141 GTGCTGCTGCTGCTCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1140
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 QY 1321 CTGTGCGCGCTGAG 1353
 Db 1321 CTGTGCGCGCTGAG 1353

RESULT 4
 US-10-305-720-1181
 ; Sequence 1181, Application US/10305720
 ; Publication No. US20040010136A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
 ; FILE REFERENCE: PA-0002-1-CON
 ; CURRENT APPLICATION NUMBER: US/10/305,720
 ; PRIORITY FILING DATE: 2002-11-26
 ; PRIORITY FILING NUMBER: 09/016,434
 ; NUMBER OF SEQ ID NOS: 1490
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1181
 ; LENGTH: 2072
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
 US-10-305-720-1181

Query Match 99.8%; Score 1349.8; DB 12; Length 2072;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 151; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACACACGAG 60
 Db 413 ATGACACACGAG 472

QY 61 TTCTCATTTCTTTTACATCTTGGGCAAGCTGTGATCACTGGCTGTGTTACAGAC 120
 Db 473 TTCTCATTTCTTTTACATCTTGGGCAAGCTGTGATCACTGGCTGTGTTACAGAC 532
 QY 121 GCGTGTGGGAG 180
 Db 533 GCGTGTGGGAG 592
 QY 181 GTGGCAAGCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
 Db 593 GTGGCAAGCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 652
 QY 241 GGGCAG 300
 Db 653 GGGCAG 712
 QY 301 GTGGCAAGCTGTGGAG 360
 Db 713 GTGGCAAGCTGTGGAG 772
 QY 361 AACTCAAG 420
 Db 773 AACTCAAG 832
 QY 421 GCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 Db 833 GCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
 QY 481 GCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 Db 893 GCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 952
 QY 541 TTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 Db 953 TTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1012
 QY 601 GCGAG 660
 Db 1013 GCGAG 1072
 QY 661 GCGAG 720
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 Db 1313 GAAG 1372
 QY 961 TCAGCTTGACAGCCCGGCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 Db 1373 TCAGCTTGACAGCCCGGCTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1432
 QY 1021 GGGCAGGTGCTCCCTGGGACAGGGGCTGGGCTGTAAGTGGGCAAGTGGGCTGAGAGAG 1080
 Db 1433 GGGCAGGTGCTCCCTGGGACAGGGGCTGGGCTGTAAGTGGGCAAGTGGGCTGAGAGAGAG 1492
 QY 1081 GCGCAGCTGACCCGAG 1140
 Db 1493 GCGCAGCTGACCCGAG 1552

| | | | |
|----|------|---|------|
| Oy | 1141 | TGCGCTGTGGTATCCCTTCCTTTCTTGAGCTACAGCAAGCCTGGCGGCATCTGGCCGAAGAC | 1200 |
| Dd | 1553 | GTCCTGTCTGTGATCCCTTCCTTTCTTGAGCTACAGCAAGCCTGGCGGCATCTGGCCGAAGAC | 1612 |
| Oy | 1201 | TGCAAGGTGCCCATATGAGCTCTTCAGATTCTTCTTGAGATCGGCTACATGCAAGACTCA | 1260 |
| Dd | 1613 | TGCAAGGTGCCCATATGAGCTCTTCAGATTCTTCTTGAGATCGGCTACATGCAAGACTCA | 1672 |
| Oy | 1261 | CTGAACCTGTTATCTACACATCTTCAACCAAGAATTCCGCGCTTCTCGGAGATC | 1320 |
| Dd | 1673 | CTGAACCTGTTATCTACACATCTTCAACCAAGAATTCCGCGCTTCTCGGAGATC | 1732 |
| Oy | 1321 | CTGTGCGCGCGGTGGAGCCAGACGGCGTGTGA | 1353 |
| Dd | 1733 | CTGTGCGCGCGGTGGAGCCAGACGGCGTGTGA | 1765 |

RESULT 5
US-10-225-567A-41

```

; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

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|-----------------------|----------------------|---------------|--------------|
| Query Match | 99.8%; Score 1349.8; | DB 15; | Length 3274; |
| Best Local Similarity | 99.9%; Pred. No. 0; | | |
| Matches 1351; | Conservative 0; | Mismatches 2; | Indels 0; |
| | | Gaps | 0; |

| | | | |
|----|-----|---|-----|
| Oy | 1 | ATGAGCACACAGAACCCCTTACTCGGTGCAAGCCAGACGGGCCATAGCGGCGGCATCAACC | 60 |
| Dd | 1 | ATGAGCACACAGAACCCCTTACTCGGTGCAAGCCAGACGGGCCATAGCGGCGGCATCAACC | 60 |
| Oy | 61 | TTCTCATATCTCTTAACAATCTTGGCAAAGCTCTGTGATCTCTGTGTGATCAACAGC | 120 |
| Dd | 61 | TTCTCATATCTCTTAACAATCTTGGCAAAGCTCTGTGATCTCTGTGTGATCAACAGC | 120 |
| Oy | 121 | CGCTGCTGCGCGGCCCTCAGAACTGTTCCGTGAGTGGCTGAGCGCGCGCGACATCTGTG | 180 |
| Dd | 121 | CGCTGCTGCGCGGCCCTCAGAACTGTTCCGTGAGTGGCTGAGCGCGCGCGACATCTGTG | 180 |
| Oy | 181 | GTGGCAGCTCATCATCTCCCTTCTCGCTGGCCAAAGAGCTGTGGGCTACTGTGATCTTC | 240 |
| Dd | 181 | GTGGCAGCTCATCATCTCCCTTCTCGCTGGCCAAAGAGCTGTGGGCTACTGTGATCTTC | 240 |
| Oy | 241 | CGGCGCAGCTGTGTGAGAGTGTACTGTGGCGCTCGACGATGCTCTTGTGACCTCGTCATC | 300 |
| Dd | 241 | CGGCGCAGCTGTGTGAGAGTGTACTGTGGCGCTCGACGATGCTCTTGTGACCTCGTCATC | 300 |
| Oy | 301 | GTGACACTGTGTGCATCAAGCTTGAGCGGCTTACTGAGGCGGTGAGCGCGGCTGAGATAC | 360 |
| Dd | 301 | GTGACACTGTGTGCATCAAGCTTGAGCGGCTTACTGAGGCGGTGAGCGCGGCTGAGATAC | 360 |
| Oy | 361 | AACCTCAAGCGCAACCCCGCGCGCATCAAGGTGATCATCTCTCACTGTGTGATCATTCGC | 420 |
| Dd | 361 | AACCTCAAGCGCAACCCCGCGCGCATCAAGGTGATCATCTCTCACTGTGTGATCATTCGC | 420 |
| Oy | 421 | GCGGTATCTCGCTGCGCGCCCTCATCTTAAGAGGCGACAGGCGCCCAAGCGCGCGG | 480 |

| | | | |
|---|------|---|------|
| Db | 421 | GGCGTCACTCGCTGCGGCCCTTATCTAACAAAGGGGACCAAGGGGCCCAAGCGCGCGGG | 480 |
| QY | 481 | CGCCCCCAGTGCAGACTCAACCAAGAGGCGCTGGTCAATCTGGCTCCAGCATCGGATCT | 540 |
| Db | 481 | CGCCCCCAGTGCAGACTCAACCAAGAGGCGCTGGTCAATCTGGCTCCAGCATCGGATCT | 540 |
| QY | 541 | TTCTTTGGCTCGTGGCTCATCATCATGATCCMTGGCTCACTCGGCGATCTCACTGGCCAA | 600 |
| Db | 541 | TTCTTTGGCTCGTGGCTCATCATCATGATCCMTGGCTCACTCGGCGATCTCACTGGCCAA | 600 |
| QY | 601 | CGCAGCAACCCGACAGAGTCCACGAGGCGCAAGGGGGGGCGTGGCAGGGTGAAGTCCAGAC | 660 |
| Db | 601 | CGCAGCAACCCGACAGAGTCCACGAGGCGCAAGGGGGGGCGTGGCAGGGTGAAGTCCAGAC | 660 |
| QY | 661 | CCCCGACCCGACCATGTGGTGGGGCTTTGGCTTCAGCCCAACTGCGCAGCCCTTGCGCTGTG | 720 |
| Db | 661 | CCCCGACCCGACCATGTGGTGGGGCTTTGGCGCTTCAGCCCAACTGCGCAGCCCTTGCGTG | 720 |
| QY | 721 | GCTTCTGCGACAGAGAGTCAACGGAACCTCGAAGTCACTGGGGGAGAGAGAGAGGGGGAG | 780 |
| Db | 721 | GCTTCTGCGACAGAGAGTCAACGGAACCTCGAAGTCACTGGGGGAGAGAGAGAGGGGGAG | 780 |
| QY | 781 | AACCCCTGAAGATACCTGGGACCCGGGCGCTTGCCACACCATGTGGGGCTGCCCTCCCACTCA | 840 |
| Db | 781 | AACCCCTGAAGATACCTGGGACCCGGGCGCTTGCCACACCATGTGGGGCTGCCCTCCCACTCA | 840 |
| QY | 841 | GCGCCAGGGCCAGAAAGAGGGGTGTTGTGGGGGACATCTCCAGAGATGAAGCTGAAGAGAG | 900 |
| Db | 841 | GCGCCAGGGCCAGAAAGAGGGGTGTTGTGGGGGACATCTCCAGAGATGAAGCTGAAGAGAG | 900 |
| QY | 901 | GAAAGAGAGAGAGAGAGAGAGAAAGATGTGAACCCCAAGGCAAGTGCAGTGTCTCGGCC | 960 |
| Db | 901 | GAAAGAGAGAGAGAGAGAGAGAAAGATGTGAACCCCAAGGCAAGTGCAGTGTCTCGGCC | 960 |
| QY | 961 | TCAGCTTGCAGGCCCCCGCTGTCAGAGCCACAGAGGCTCCGGGGTGTGGCCACCTACGT | 1020 |
| Db | 961 | TCAGCTTGCAGGCCCCCGCTGTCAGAGCCACAGAGGCTCCGGGGTGTGGCCACCTACGT | 1020 |
| QY | 1021 | GCGCCAGTGTCTCTGCGGACGGGGCGTGGTGTATAGTGGGAGTGGGAGATGTGGCGTGAAG | 1080 |
| Db | 1021 | GCGCCAGTGTCTCTGCGGACGGGGCGTGGTGTATAGTGGGAGTGGGAGATGTGGCGTGAAG | 1080 |
| QY | 1081 | GCGCAGCTGACCCCGGAGAAAGGGCTTCAACCTTCGTCGTCGGCTGTGTCATTTGGCGTTTT | 1140 |
| Db | 1081 | GCGCAGCTGACCCCGGAGAAAGGGCTTCAACCTTCGTCGTCGGCTGTGTCATTTGGCGTTTT | 1140 |
| QY | 1141 | GGGCTCTGCTGGTCCCCCTCTTCTTCAAGCTACAGGCTGGGGGCGCATCTGGCCGAAGCAC | 1200 |
| Db | 1141 | GGGCTCTGCTGGTCCCCCTCTTCTTCAAGCTACAGGCTGGGGGCGCATCTGGCCGAAGCAC | 1200 |
| QY | 1201 | TGCAGAGTGCAGCATGGGCTCTTCCAGTTCCTTCTTGATCGGCTAGCTGCAACAGCTCA | 1260 |
| Db | 1201 | TGCAGAGTGCAGCATGGGCTCTTCCAGTTCCTTCTTGATCGGCTAGCTGCAACAGCTCA | 1260 |
| QY | 1261 | CTGAACCTCTGTATCTACACCATCTTCAACCAAGAGACTTCGCGCGTCCCTTCCGGAAGATC | 1320 |
| Db | 1261 | CTGAACCTCTGTATCTACACCATCTTCAACCAAGAGACTTCGCGCGTCCCTTCCGGAAGATC | 1320 |
| QY | 1321 | CTGTGCGCGCGGTGAGCCAGACGGGCTGGTA | 1353 |
| Db | 1321 | CTGTGCGCGCGGTGAGCCAGACGGGCTGGTA | 1353 |
| RESULT 6 | | | |
| US-10-001-073-2 | | | |
| ; Sequence 2, Application US/10001073 | | | |
| ; Publication No. US20030113725A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Liggett, Stephen | | | |
| ; APPLICANT: Small, Kirsten | | | |
| ; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms | | | |
| ; FILE REFERENCE: 13073-PCT | | | |

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/ CURRENT APPLICATION NUMBER: US/10/001.073
/ CURRENT FILING DATE: 2001-11-01
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 1344
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-001-073-2

Query Match      97.9%; Score 1325; DB 15; Length 1344;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;

QY 1 ATGACACACGAGAGACCCCTACTCGTGCAGAGCCACAGCCGACATAGCGGCGCATACC 60
DB 1 ATGACACACGAGAGACCCCTACTCGTGCAGAGCCACAGCCGACATAGCGGCGCATACC 60
QY 61 TTCTCATTTCTTTTACATCTTTCGCGACGCTCTGATCACTCTGCTGTGTGACACAG 120
DB 61 TTCTCATTTCTTTTACATCTTTCGCGACGCTCTGATCACTCTGCTGTGTGACACAG 120
QY 121 CGCTCGCTGCGCCCTCTGAAACCTGTTCTGTGTGTCTGCTGCGCCGCGCATCTG 180
DB 121 CGCTCGCTGCGCCCTCTGAAACCTGTTCTGTGTGTCTGCTGCGCCGCGCATCTG 180
QY 181 GTGACACGCTCATCATCTCTTCTGCTGCGACAGAGCTGTGGGCTACTGTGATCTTC 240
DB 181 GTGACACGCTCATCATCTCTTCTGCTGCGACAGAGCTGTGGGCTACTGTGATCTTC 240
QY 241 CGGCGACGCTGATGCGAGGTGTA CTTGCGCTGCGAGCTGCTCTTCTGCACTTCGTCATC 300
DB 241 CGGCGACGCTGATGCGAGGTGTA CTTGCGCTGCGAGCTGCTCTTCTGCACTTCGTCATC 300
QY 301 GTGACACTGTGCGCCCATCAGCTTGACCGCTTACTGCGCGCTGAGCCGCGCTGTGATAC 360
DB 301 GTGACACTGTGCGCCCATCAGCTTGACCGCTTACTGCGCGCTGAGCCGCGCTGTGATAC 360
QY 361 AACTCCAAAGGCGACCCCGCGCGCATCAAGTGTGATCATCTCACTGTGTGCTCATCGCC 420
DB 361 AACTCCAAAGGCGACCCCGCGCGCATCAAGTGTGATCATCTCACTGTGTGCTCATCGCC 420
QY 421 GCGGTATCTGCTGCGCCCTCATCTTACAGGCGACCAAGGCGCCCAAGCCGCGCGG 480
DB 421 GCGGTATCTGCTGCGCCCTCATCTTACAGGCGACCAAGGCGCCCAAGCCGCGCGG 480
QY 481 CGCCCCCAGTGCAGAGCTCAACAGAGGCTGTGATCTCTGCTCTCCAGCATCGATCT 540
DB 481 CGCCCCCAGTGCAGAGCTCAACAGAGGCTGTGATCTCTGCTCTCCAGCATCGATCT 540
QY 541 TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTACCTGATCGCCAA 600
DB 541 TTCTTGTCTCTGCTCATCATGATCTTGTCTACCTGCGCATCTACCTGATCGCCAA 600
QY 601 CGGAGCAACCGCAGAGGTCCAGAGGCGCAAGGCGGCGCTGTGCGAGGATGTCAGAG 660
DB 601 CGGAGCAACCGCAGAGGTCCAGAGGCGCAAGGCGGCGCTGTGCGAGGATGTCAGAG 660
QY 661 CCCCGACCCGACCATGTGTGGGCTTTGGCTTCAGCCAACTGCAACCTGTGGCTCTGTG 720
DB 661 CCCCGACCCGACCATGTGTGGGCTTTGGCTTCAGCCAACTGCAACCTGTGGCTCTGTG 720
QY 721 GCTTTCGCGAGAGGTCAACGAGCACTGGAAGTCACTGAGGAGAGAGAGAGAGAGAG 780
DB 721 GCTTTCGCGAGAGGTCAACGAGCACTGGAAGTCACTGAGGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTGGAAGATACCTGGAACCCGCGCTTGCACCCAGTTGGGCTCCCTTCCCACTCA 840
DB 781 ACCCTGGAAGATACCTGGAACCCGCGCTTGCACCCAGTTGGGCTCCCTTCCCACTCA 840
QY 841 GCGCAGGCGCAGAGAGGCTTTTGTGGGCTCTTCCAGAGATGAAGCTGAAGAGAG 900
DB 841 GCGCAGGCGCAGAGAGGCTTTTGTGGGCTCTTCCAGAGATGAAGCT----- 891
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QY 901 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 892 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 951
QY 961 TCAGCTTGAGCCGCCCGCTGCGAGCAGCCAGAGGCTCCCGGATGCTGAGCCACCTTACGT 1020
DB 952 TCAGCTTGAGCCGCCCGCTGCGAGCAGCCAGAGGCTCCCGGATGCTGAGCCACCTTACGT 1011
QY 1021 GGCAGAGTCTCTTGGGAGAGGCGCTGTGCTTATAGTGGGAGTGTGGGTGAGAG 1080
DB 1012 GGCAGAGTCTCTTGGGAGAGGCGCTGTGCTTATAGTGGGAGTGTGGGTGAGAG 1071
QY 1081 GGCAGAGTACCCCGGAGAGAGGCTTCACTTGTGCTGCTGTGCTGCTTGTGCTTTT 1140
DB 1072 GGCAGAGTACCCCGGAGAGAGGCTTCACTTGTGCTGCTGTGCTGCTTGTGCTTTT 1131
QY 1141 GTGCTGTGCTGCTTCCCTTCTTCTTCAAGCTACAGCTGTGGGCGCATCTGCGAGAC 1200
DB 1132 GTGCTGTGCTGCTTCCCTTCTTCTTCAAGCTACAGCTGTGGGCGCATCTGCGAGAC 1191
QY 1201 TGCAGAGTCCCGCATAGGCTCTTCCAGTCTTCTTGTGATGTGCTACAGAGCTCA 1260
DB 1192 TGCAGAGTCCCGCATAGGCTCTTCCAGTCTTCTTGTGATGTGCTACAGAGCTCA 1251
QY 1261 CTGAACCTGTATCTACACATCTTCAACAGAGCTTCCGCGCTTCCGAGAGATC 1320
DB 1252 CTGAACCTGTATCTACACATCTTCAACAGAGCTTCCGCGCTTCCGAGAGATC 1311
QY 1321 CTGTGCGCGCGCTGAGACCCAGACGCGCTGTGTA 1353
DB 1312 CTGTGCGCGCGCTGAGACCCAGACGCGCTGTGTA 1344
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RESULT 7
US-09-825-923-1
/ Sequence 1, Application US/09825923
/ Patent No. US2001001638A1
/ GENERAL INFORMATION:
/ APPLICANT: Snapir, Amir
/ APPLICANT: Heinonen, Paula
/ APPLICANT: Alhopuro, Pia
/ APPLICANT: Karvonen, Matti
/ APPLICANT: Koulu, Markku
/ APPLICANT: Pesonen, Ullamari
/ APPLICANT: Scheinin, Mika
/ APPLICANT: Salonen, Jukka T
/ APPLICANT: Tuomala, Tomi-Pekka
/ APPLICANT: Lakka, Timo A
/ APPLICANT: Myllynen, Kristina
/ APPLICANT: Salonen, Riitta
/ APPLICANT: Kaunonen, Jussi
/ APPLICANT: Valkonen, Veli-Pekka
/ TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
/ FILE REFERENCE: Alpha-2B-AR variant
/ CURRENT APPLICATION NUMBER: US/09/825,923
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 09/422,985
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1344
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: CDS
/ LOCATION: (1) .. (1341)
/ OTHER INFORMATION: Coding sequence for variant human
/ OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1
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Query Match 97.8%; Score 1323.4; DB 9; Length 1344;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 ATGAGACACCAAGAGACCCCTTACTCCGTGACAGGCCCAAGCGGCATAGCGGGGCATACACC 60
DB 1 ATGAGACACCAAGAGACCCCTTACTCCGTGACAGGCCCAAGCGGCATAGCGGGGCATACACC 60
QY 61 TTCCTCATTTCTTTTACCATCTTCCGCAAGCTCTGATCTCTGGCTGTTGACACAG 120
DB 61 TTCCTCATTTCTTTTACCATCTTCCGCAAGCTCTGATCTCTGGCTGTTGACACAG 120
QY 121 CGCTGCTGCGCGCCCTTCAAGAACTGTTCTGCTGCTGCTGCGCGCGCGCAATCTTG 180
DB 121 CGCTGCTGCGCGCCCTTCAAGAACTGTTCTGCTGCTGCTGCGCGCGCGCAATCTTG 180
QY 181 GTGGCCAGCTCATATCCCTTTCTGCTGCGCAAGAGCTGCTGGGCTTACTGTAATTG 240
DB 181 GTGGCCAGCTCATATCCCTTTCTGCTGCGCAAGAGCTGCTGGGCTTACTGTAATTG 240
QY 241 CGGCGCAGCTGTCAGAGGTATCTGCGCTGCAAGTGTCTTTCGACCTGTCATC 300
DB 241 CGGCGCAGCTGTCAGAGGTATCTGCGCTGCAAGTGTCTTTCGACCTGTCATC 300
QY 301 GTGCACTGTGCGCATCAAGCTTGAACCGCTACTGCGCGCTGAGCCGCGCTGAGTAC 360
DB 301 GTGCACTGTGCGCATCAAGCTTGAACCGCTACTGCGCGCTGAGCCGCGCTGAGTAC 360
QY 361 AACTCCAGCGCAACCCCGCGCGCGCATCAAGTGCATATCTCTGCTGCTGCTGCTGCC 420
DB 361 AACTCCAGCGCAACCCCGCGCGCGCATCAAGTGCATATCTCTGCTGCTGCTGCTGCC 420
QY 421 GCGCTATCTGCTGCGCGCGCGCATCTCAAGGGGAGACAGGCCCGCGCGCGCGCG 480
DB 421 GCGCTATCTGCTGCGCGCGCGCATCTCAAGGGGAGACAGGCCCGCGCGCGCGCGCG 480
QY 481 CGCCCCCAGTGCAGCTCAACAGAGGCTGTATCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 CGCCCCCAGTGCAGCTCAACAGAGGCTGTATCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 TTCTTTGCTCTTCTGCTCATATGATCTTGTCTACCTGCGCATCTACTGATCGCAAA 600
DB 541 TTCTTTGCTCTTCTGCTCATATGATCTTGTCTACCTGCGCATCTACTGATCGCAAA 600
QY 601 CGCAGAACCGCAGAGTCCCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 CGCAGAACCGCAGAGTCCCAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 CCCCGACCCGACCATGCTGAGGCTTGGCTGCTGAGCCAACTGCGCAGCCGCGCGCTGTG 720
DB 661 CCCCGACCCGACCATGCTGAGGCTTGGCTGCTGAGCCAACTGCGCAGCCGCGCGCTGTG 720
QY 721 GCTTTCGACAGAGGTCAACGCACTCGAAGTCACTGGGAGAGAGAGAGAGAGAGAGAG 780
DB 721 GCTTTCGACAGAGGTCAACGCACTCGAAGTCACTGGGAGAGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAAAGATATCTGGGACCCGCGCGCTTGGCAACCAAGTTGGCTGCTTCCCACTCA 840
DB 781 ACCCTGAAAGATATCTGGGACCCGCGCGCTTGGCAACCAAGTTGGCTGCTTCCCACTCA 840
QY 841 GGCAGAGGACAG 900
DB 841 GGCAGAGGACAG 900
QY 901 GAAAG 960
DB 901 GAAAG 960
QY 961 TGAAGCTTGAAGCCCCCGCTGACAGCAACAGAGGCTCCCGGGTGTGCGACCTTACCT 1020
DB 961 TGAAGCTTGAAGCCCCCGCTGACAGCAACAGAGGCTCCCGGGTGTGCGACCTTACCT 1020
QY 1021 GGCAGAGTCTCTGCG 1080
DB 1021 GGCAGAGTCTCTGCG 1080

DB 1012 GGCAGAGTCTCTGCG 1071
QY 1081 GGCAGAGTCTCTGCG 1140
DB 1072 GGCAGAGTCTCTGCG 1131
QY 1141 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1132 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
QY 1201 TGCAGAGTCCCGCAGAGGCTCTTTCAGATTCTTCTTTCAGATGCGCTACGCAACAGCTCA 1260
DB 1192 TGCAGAGTCCCGCAGAGGCTCTTTCAGATTCTTCTTTCAGATGCGCTACGCAACAGCTCA 1251
QY 1261 CTGAACCTCTGATCTCAACACATCTTCAACAGAGACTTCCCGCGCTGCGAGAGATC 1320
DB 1252 CTGAACCTCTGATCTCAACACATCTTCAACAGAGACTTCCCGCGCTGCGAGAGATC 1311
QY 1321 CTGTGCG 1353
DB 1312 CTGTGCG 1344

RESULT 8
US-10-077-870-1
; Sequence 1, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salomon, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

Query Match 97.8%; Score 1323.4; DB 15; Length 1344;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 ATGAGACACCAAGAGACCCCTTACTCCGTGACAGGCCCAAGCGGCATAGCGGGGCATACACC 60
DB 1 ATGAGACACCAAGAGACCCCTTACTCCGTGACAGGCCCAAGCGGCATAGCGGGGCATACACC 60
QY 61 TTCCTCATTTCTTTTACCATCTTCCGCAAGCTCTGATCTCTGGCTGTTGACACAG 120
DB 61 TTCCTCATTTCTTTTACCATCTTCCGCAAGCTCTGATCTCTGGCTGTTGACACAG 120
QY 121 CGCTGCTGCGCGCCCTTCAAGAACTGTTCTGCTGCTGCTGCGCGCGCGCAATCTTG 180
DB 121 CGCTGCTGCGCGCCCTTCAAGAACTGTTCTGCTGCTGCTGCGCGCGCGCAATCTTG 180
QY 181 GTGGCCAGCTCATATCCCTTTCTGCTGCGCAAGAGCTGCTGGGCTTACTGTAATTG 240
DB 181 GTGGCCAGCTCATATCCCTTTCTGCTGCGCAAGAGCTGCTGGGCTTACTGTAATTG 240
QY 241 CGGCGCAGCTGTCAGAGGTATCTGCGCTGCAAGTGTCTTTCGACCTGTCATC 300
DB 241 CGGCGCAGCTGTCAGAGGTATCTGCGCTGCAAGTGTCTTTCGACCTGTCATC 300
QY 301 GTGCACTGTGCGCATCAAGCTTGAACCGCTACTGCGCGCTGAGCCGCGCTGAGTAC 360
DB 301 GTGCACTGTGCGCATCAAGCTTGAACCGCTACTGCGCGCTGAGCCGCGCTGAGTAC 360

Db 301 GTGCACTTGTGGCCATCAGCTCGACCGGTGAGTGGCCGCTGAGTAC 360
Qy 361 AACTCAAGGCGACCCCGCGCGCATGAGTGCATCTCTCTGTGTGCTCATCGCC 420
Db 361 AACTCAAGGCGACCCCGCGCGCATGAGTGCATCTCTCTGTGTGCTCATCGCC 420
Qy 421 GCGGTATCTGCTGCGCGCGCATCTCTCAAGGCGCGCATCGCGCGCGCGCG 480
Db 421 GCGGTATCTGCTGCGCGCGCATCTCTCAAGGCGCGCATCGCGCGCGCGCG 480
Qy 481 CGCGCCAGTGCAGAGTGCACAGAGGCGCTGTGATCTCTGCTTCAGATCGATCT 540
Db 481 CGCGCCAGTGCAGAGTGCACAGAGGCGCTGTGATCTCTGCTTCAGATCGATCT 540
Qy 541 TTCTTTGCTCTCTGCTCATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TTCTTTGCTCTCTGCTCATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Qy 601 CGGAGAACCGGAGAGTCCGAGGCGCAAGGCGCGCGCTGCGAGGAGTGCATGAG 660
Db 601 CGGAGAACCGGAGAGTCCGAGGCGCAAGGCGCGCGCTGCGAGGAGTGCATGAG 660
Qy 661 CCCGACCCGACCATGCTGCGCGCTTTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 CCCGACCCGACCATGCTGCGCGCTTTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 721 GCTTCTGCGAGAGTGCACAGGCACTCTGAGTGCAGTGCAGGAGAGGAGGAG 780
Db 721 GCTTCTGCGAGAGTGCACAGGCACTCTGAGTGCAGTGCAGGAGAGGAGGAG 780
Qy 781 ACCCTGAGAGTATCTGAGGAGCCGCGCGCTTGCACCCGAGTGGCTGCTTCCCACTCA 840
Db 781 ACCCTGAGAGTATCTGAGGAGCCGCGCGCTTGCACCCGAGTGGCTGCTTCCCACTCA 840
Qy 841 GGCAGGCGCGAGAGGAGGCTTTGCTGCGGCACTCTGAGAGTGAAGTGAAGAG 900
Db 841 GGCAGGCGCGAGAGGAGGCTTTGCTGCGGCACTCTGAGAGTGAAGTGAAGAG 900
Qy 901 GAGAGAGAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960
Db 901 GAGAGAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960
Qy 961 TCAGCTTGCAGCGCGCGCTGCGAGGCGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
Db 961 TCAGCTTGCAGCGCGCGCTGCGAGGCGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
Qy 1021 GGCAGGCTGCTGCTGCGAGGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
Db 1021 GGCAGGCTGCTGCTGCGAGGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
Qy 1081 GCGCAGTGCACCGCGGAGAGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1081 GCGCAGTGCACCGCGGAGAGGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Qy 1141 GTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 GTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Qy 1201 TGCAAGGTGCGCGAGTGCCTTTCAGTTCCTTTCAGTTCCTTTCAGTTCCTT 1260
Db 1201 TGCAAGGTGCGCGAGTGCCTTTCAGTTCCTTTCAGTTCCTTTCAGTTCCTT 1260
Qy 1261 CTGAACCTGCTTATCTAATCTTCAACCTTCAACCTTCAACCTTCAACCTTCA 1320
Db 1261 CTGAACCTGCTTATCTAATCTTCAACCTTCAACCTTCAACCTTCAACCTTCA 1320
Qy 1321 CTGAGCGCGCGAGAGTGCAGAGGCGCTGAGTGA 1383
Db 1321 CTGAGCGCGCGAGAGTGCAGAGGCGCTGAGTGA 1383
Qy 1383 CTGAGCGCGCGAGAGTGCAGAGGCGCTGAGTGA 1383
Db 1383 CTGAGCGCGCGAGAGTGCAGAGGCGCTGAGTGA 1383

US-10-311-455-48/c
; Sequence 48, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIERENBERG, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 48
; LENGTH: 6904
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: 821
; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-48

Query Match 44.4%; Score 600.2; DB 13; Length 6904;
Best Local Similarity 75.8%; Pred. No. 1.2e-137;
Matches 759; Conservative 0; Mismatches 233; Indels 9; Gaps 1;

Qy 1 ATGACACACAGAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1904 ATGACACACAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1845
Qy 61 TTCTTCATCTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 120
Db 1844 TTCTTCATCTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 1785
Qy 121 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 1784 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1725
Qy 181 GTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 1724 GTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665
Qy 241 CGGCGAGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
Db 1664 CGGCGAGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1605
Qy 301 GTGACAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAG 360
Db 1604 GTGACAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAG 1545
Qy 361 AACTCAAGGCGACCCCGCGCGCATGAGTGCATCTCTCTGTGTGCTCATCGCC 420
Db 1544 AACTCAAGGCGACCCCGCGCGCATGAGTGCATCTCTCTGTGTGCTCATCGCC 1485
Qy 421 GCGGTATCTGCTGCGCGCGCATCTCTCAAGGCGCGCATCGCGCGCGCGCGCG 480
Db 1484 GCGGTATCTGCTGCGCGCGCATCTCTCAAGGCGCGCATCGCGCGCGCGCGCG 1425
Qy 481 CGCGCCAGTGCAGAGTGCACAGAGGCGCTGTGATCTCTGCTTCAGATCGATCT 540
Db 1424 CGCGCCAGTGCAGAGTGCACAGAGGCGCTGTGATCTCTGCTTCAGATCGATCT 1365
Qy 541 TTCTTTGCTCTCTGCTCATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TTCTTTGCTCTCTGCTCATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600


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; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-40

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| | | | | | | | |
|-----------------------|--------|--------------|----------|------------|-----|--------|-------|
| Query Match | 33.9%; | Score | 458.4; | DB | 15; | Length | 1386; |
| Best Local Similarity | 62.6%; | Pred. No. | 6.7e-103 | | | | |
| Matches | 82; | Conservative | 0; | Mismatches | 41; | Indels | 84; |
| | | | | | | Gaps | 4 |

[illegible]

| | | | |
|----|------|--|------|
| OY | 913 | GAGAGAGAGAGAGAGTGTGAACCCAGGAGAGTGCAGTGTCTTCGCGCTCAGCTTCGAGC | 972 |
| Db | 967 | GCGGGAGCCGGGGGCGGCTGAAGTGGGGGGCGCTGACCGGCTCCAGGTCCCGGGGCCGGT | 1026 |
| OY | 973 | CCCCCGCTGCAGACGCCACAGGGCTCCGGGTCTGGCCACCCTTAGTGGCCAGGTGTCTC | 1032 |
| Db | 1027 | GGCGCGCTCTTCGCGCGCCAGACTGCGCGTCCGTGAGATTCTTCGTGCGCCCGCGCGGG | 1086 |
| OY | 1033 | CTGGGCGAGGGGCGGTGGGTGTATATAGTGGCAGTGGTGGCGGTGAAAGGGCGCAGCTTACC | 1092 |
| Db | 1087 | GCGGCGAGCAGCGT-----GTGCGCGCGCAGAGTGGGCCAGGGCG | 1125 |
| OY | 1093 | CGGAGAGAGCGCTTCACTTCGTGCTGGCTGTGGTCAATTGGCTTTTGTGTCTCTGTGG | 1152 |
| Db | 1126 | CGGAGAGAGCGCTTCACTTGTGTCTGGCTGTGGTCAATGGGCGGTGTCTGTGTGTGG | 1185 |
| OY | 1153 | TTCCCTCTTCTTCTCAGCTACAGCGCTGGGGGCCCATCGGCCGGAAGCATGCGAAGGTGCC | 1212 |
| Db | 1186 | TTCCCTCTTCTTCTCAGCTACAGCGCTGAGCGCATCTGCGCGCAGAGGCTGCGAGTGC | 1245 |
| OY | 1213 | CATGAGCTCTTCCAGTTCCTTCTTGATCGGCTACTGCAACAGCTCATGAACTCTGTT | 1272 |
| Db | 1246 | GAGCCGCTCTTCAAGTTCTTCTTGATCGGCTACTGCAACAGCTCATGAACTCTGTT | 1305 |
| OY | 1273 | ATTCAACCAATCTTCAACCAAGACTTCCGCGGTGCTTCGGAGAGATCTGTGCGCGCGG | 1332 |
| Db | 1306 | ATTCAACCAAGTCTTCAACCAAGATTTCCGCGCATCTTCAAGCAACATCTCTTCCGACGG | 1365 |
| OY | 1333 | TGGA | 1336 |
| Db | 1366 | AGGA | 1369 |

```

RESULT 12
US-10-001-073-42
: Sequence 42, Application US/10001073
: Publication No. US20030113725A1
: GENERAL INFORMATION:
: APPLICANT: Isggett, Stephen
: APPLICANT: Small, Kirsten
: TITLE OF INVENTION: Alpha-a-adrenergic re
: FILE REFERENCE: 13073-PCT
: CURRENT APPLICATION NUMBER: US/10/001,073
: CURRENT FILING DATE: 2001-11-01
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn Ver. 2.0
: SEQ. ID NO 42
: LENGTH: 1374
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-001-073-42

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| | | | | | | | |
|-------------|-------|--------------|----------|------------|-----|--------|------|
| Query Match | 33.2% | Score | 448.8 | DB | 15 | Length | 1374 |
| Similarity | 62.4% | Pred. No. | 1.5e-100 | | | | |
| Matches | 826 | Conservative | 0 | Mismatches | 402 | Indels | 96 |
| | | | | | | Gaps | 4 |

[illegible]

Db 370 TGGGGGCTGTAACCTGGCGCTGATGCTGTTTGGACCTCGGATCGATCGTGTCTGTGT 429
Qy 313 GCCATGAGCTGGACCGCTACTGAGCGGAGCGCGCTGGAGTCAACCTCAAGCGC 372
Db 430 GCCATGAGCTGGACCGCTACTGAGCGGAGCGCGCTGGAGTCAACCTCAAGCGC 489
Qy 373 ACCCGCGCGCGCATCAAGTGCATCTCACTGTGTGCTCATCGCGCGCTCATCTCG 432
Db 490 AACACCGCGCGCTCAAGGCGACATCGTGTGTGTGTCTCATCTCGCGCTCATCTCG 549
Qy 433 CTGCGCGCGCTCATCTCAAGGCGACGAGGCGCGCGCGCGCGCGCGCGCGCGCG 492
Db 550 TTCCCGCGCGCTGTCT---CGCTCTACCGCGACCGCGCGCGCGCGCGCGCGCG 606
Qy 493 AAGCTCAACGAGAGCGCTGTGATCTCGGCTCGAGATCGGATCTTTTGTGTCTCT 552
Db 607 GGCCTCAAGAGACGAGCTGTGATCTGTCTCTGTGATCGGCTCTTTCTTGCGCGCC 666
Qy 553 TGCCTCATGATGATCTTGTCTCTACCTGCGCATCTACCTGATCGCAACGCGCAACCGC 612
Db 667 TGCCTCATGATGAGCTGTGTCTACGCGCGCATCTACGAGTGCAGAGCTGCGACGCGC 726
Qy 613 AAGAGTCCAGGCGCAAGGCGGCGCTGCGAGGCTGAGTCCAGAGCGCGCGCGCGAGC 672
Db 727 A-----CGCTCAGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 759
Qy 673 CATGTGGGGCTTTGGCGCTCAGCCAACTGCGAGCGCTGCGCTGTGTGTCTTGTGCA 732
Db 760 GACGGGTGCTCCCGCATACCGAAAAGGCGTGGGCGCGCGCGCGCGCGCGCGCGAG 819
Qy 733 GAGGTCAAGGAGACTCGAAGTCCACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
Db 820 GGGCACTGGCGAG 879
Qy 793 ACTGGAGCCCGGCGCTTGGCAACGAGTGGGCTGCCCTTCCAACTCAGGCGCGAGCG 852
Db 880 AGCGGCGCGC-----GCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Qy 853 AAGGAGGCTGTTTGTGGGCGATCTCCAGAGATGAGAGTGAAGAGAGAGAGAGAGAG 912
Db 901 TTGCGCGCGGCG 960
Qy 913 GAGGAGGAGAGAGAGTGTGAACCCAGGAGTGCAGTGTCTCGCGCTCAGCTTGACG 972
Db 961 CAGGGGCGGCTGAGTGGGCGCGCTGACCGCTCCAGGTCGCCGCGCGCGCGCGCGCG 1020
Qy 973 CCGCGCGCTCAGGAGCGCAGAGGCTCCGCGGTGTGCGCAACCTCAGTGGCGAGTGTCT 1032
Db 1021 CTCTGCGCGCGCAGCTCGCGCTCCGCTGAGTTCCTGTGCGCGCGCGCGCGCGCGCG 1080
Qy 1033 CTGGGCGAGGCGGTGGGTGCTAAGTGGGCACTGTGGCGTGAAGGCGCGAGCTGACC 1092
Db 1081 ACGAGC-----GTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1113
Qy 1093 CGGAGAGAGCGCTTCACTTGTGCTGCGGTGAGTGTGATGTGGCTTTTGTGCTGTGCG 1152
Db 1114 CGCGAGAGAGCGCTTCACTTGTGCTGCGGTGAGTGTGATGTGGCTTTTGTGCTGTGCG 1173
Qy 1153 TTCCCGCTTCTTCACTCAAGCTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1212
Db 1174 TTCCCGCTTCTTCACTCAAGCTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1233
Qy 1213 CATGCGCTTCTTCAAGTCTTCTTGTGAGTGGGTACTGCAACAGCTCACTGAACTGTT 1272
Db 1234 GCGCGCGCTTCAAGTCTTCTTGTGAGTGGGTACTGCAACAGCTCACTGAACTGTT 1293
Qy 1273 ATCTACACATCTTGAACAGAGCTTCCGCGGTGCTTCCGAGAGTCTGTGCGCGCGCG 1332
Db 1294 ATCTACACAGCTTCAACAGAGATTCGCGCATCTTCAAGAGATCTTCTTGTGCGAG 1353
Qy 1333 TGGAG 1336
|||

Db 1354 AGGA 1357
RESULT 13
US-10-225-567A-43
; Sequence 43, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 2826
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-43
Query Match 33.1%; Score 447.2; DB 15; Length 2826;
Best Local Similarity 62.6%; Pred. No. 4,2e-100;
Matches 829; Conservative 0; Mismatches 408; Indels 87; Gaps 5;
Qy 13 GACCCCTACTCCGTGAGGCGCAAGCGCGCATAGCGGCGCGCATCACTTCTCATTTCTC 72
Db 1021 GGCAGTACTCG 1080
Qy 73 TTACCATTTTGGCAACGCTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 132
Db 1081 TTACCATTTTGGCAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
Qy 133 GCCCTCAGAACCTGTCTGT 192
Db 1141 GCGCAGAACACCTTCTTGT 1200
Qy 193 ATCATCCCTTCTTGT 252
Db 1201 GTCATGCCCTTCTTGT 1260
Qy 253 TCGAGGTGTACCTGTGCGCTGACGCTCTTCTGTGACCTGTGTGTGTGTGTGTGTGTGT 312
Db 1261 TCGGGGTGTACTGTGCGCTGACGCTCTTCTGTGACCTGTGTGTGTGTGTGTGTGTGT 1320
Qy 313 GCCATGAGCTTGAACCGCTACTGTGGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCG 372
Db 1321 GCCATGAGCTTGAACCGCTACTGTGGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Qy 373 ACCCGCGCGCGCATCAAGTGCATCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 432
Db 1381 AACACCGCGCGCTCAAGGCGACATCTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
Qy 433 CTGCGCGCGCTCATCTCAAGGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 492
Db 1441 TTCCCGCGCGCTGTCT---CGCTCTACCGCGACCGCGCGCGCGCGCGCGCGCGCGCG 1497
Qy 493 AAGCTCAACGAGAGCGCTGTGATCTGTGCGCTTCAAGATGTGATCTTTTGTGTCTCT 552
Db 1498 GGCCTCAAGAGAGAGCTGTGATCTGTGCGCTTCAAGATGTGATCTTTTGTGTCTCT 1557
Qy 553 TGCCTCATGATGATCTTGTCTTACCTGCGCATCTACCTGATGCGCAACGCGCAACCGCG 612
Db 1558 TGCCTCATGATGAGCTGTGTCTACGCGCGCATCTACGAGTGCAGAGGTGTGCGAGCGCG 1617
Qy 613 AAGAGTCCAGGCGCAAGGCGGCGCGCTGCGGCAAGGCTGAGTCCAGAGCGCGCGAGCG 672
Db 1618 A-----CGCTCAGCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1667

| | | | | |
|----|------|--|--------------------------------|------|
| Db | 1083 | AGCAGC----- | -----GTCGTCCCCCGCAAGTGGCCAGGCG | 1115 |
| Qy | 1093 | CGGGAGAAAGCGCTTCACCTTCGTGCTGGCTGTGTCATTCGACGTTTTGTGCTCTGCTGG | | 1152 |
| Db | 1116 | CGCGAGAAAGCGCTTCACCTTGTGTGCTGGCTGTGGTCATGAGGTGTGTGTCCTCTGCTGG | | 1175 |
| Qy | 1153 | TTCCCGCTTCCTTCAGCTACAGCGCTGGGGCCCATCTGCGCCGGAAGCACTGCAAGGTGCCC | | 1212 |
| Db | 1176 | TTCCCGCTTCCTTCAGCTACAGCGCTGTACGGCATTCTGCCCGAGGCTTGCAGAGTGCCTC | | 1235 |
| Qy | 1213 | CATGGCCCTTCCTTCAGTTCCTTCCTGATTCGGCTACTGCAACAGCTCACTGAACCTCTGT | | 1272 |
| Db | 1236 | GGCCCGCTTCCTTCAGTTCCTTCCTGATTCGGCTACTGCAACAGTCCCTCAACCCGCTC | | 1295 |
| Qy | 1273 | ATCTACACCACTTCACACCAAGACTTCCGCCGTGCTTCGGAAGGATCTGTGCCGCCG | | 1332 |
| Db | 1296 | ATCTACAGGCTTCACACCAAGATTTCCGGGATCTCTTAAGACATCTCTTCCGACGG | | 1355 |
| Qy | 1333 | TGGA | | |
| Db | 1356 | AGGA | | |

```

RESULT 15
US-10-101-510-754
Sequence 754, Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WAN, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 754
LENGTH: 1382
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-754

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|-----------------------|--------------|--------------------|-----------------|--------------|
| Query Match | 32.8%; | Score 444; | DB 13; | Length 1382; |
| Best Local Similarity | 62.2%; | Pred. No. 2.3e-99; | | |
| Matches 823; | Conservative | 0; | Mismatches 405; | Indels 96; |
| | | | | Gaps 4; |

Oy 13 GACCCTCTCTCCGTCCAGGCCACAGGGGCGCATGCGCGGCATCATCTTCATATCTC 72
 Db 132 GGGCAGTACTCGCGGGGCGGGGAGGCGAGGAGCTGGCTGCGGTGGTGGGCTTCCTCATGCTC 151
 Oy 73 TTATACATCTTCGGGCACGCTCTGTGCATCTGTGCTGTGTTACACAGCGCTGCGCTGGC 132
 Db 192 TTACACGTGTGGGGCAACGTGTGGTGGTGGATGCGCGTGTAGCACGGCGGGGCTGGCGC 251
 Oy 133 GCGCCTCAGAACCTGTCTCTGGTGTGCTGGCGCGCGCGACATCCTGTGTGGCCACGCTC 192
 Db 252 GCGGCACAGAACCTCTCTCTGGTGTGCTGGCTGGCGCGACATCCTGTGTGGCCACGCTG 311
 Oy 193 ATCATCTCTTTCTCGCTGGGCCAACAGCTGTGGGCTACTGTGTATCTTCGGGCGCAGTGG 252
 Db 312 GTCATGCCCTTCTCGTTGGGCCAACAGAGCTCATGGCTACTGTGTATCTTCGGGCGAGTGG 371
 Oy 253 TGGGAGTGTACTGGCGCTCGACAGTGTCTTTCTGCACCTGTCATCTGTGACCTGTGC 312
 Db 372 TGGGCGTGTACTGGCGCGCTCGATGTGTCTGTTTGTGACCTCGTGTGATGTGTGTGT 431
 Oy 313 GCCATCAGCGCTGGACCGCTACTGTGGGCGCTGTGAGCGCGCGCTGGAGTTCACATCCMAAGCC 372
 Db 432 GCCATCAGCGCTGGACCGCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 491

QY ACCCGGCGCCGATCAAGGATCATATCCCTCACTGATGGCTATCGCCGCGGCATCTCG 432
 Db ACACCAACCGCGGTGAAGGCCACATCGTGGCGCTGTTGGCTATCTCGGCGGTCACTCC 551
 QY CTGCGCCGCTTCATCTACAGGGGACCAAGGGCCCCAGCCGCGCGGGCGCCCCCATGTC 432
 Db TTCCCGCGCTGGTCT---CGCTCTACCGCCAGCCCGACGGGCGCGCCCTTACCCGCAATGC 608
 QY AAGCTCAACCAAGAGGCGCTGGTACATCCGGGCTCCAGCATCGGAATCTTCTTCTTGACCT 552
 Db GGCTCAACGACGAAACCTGGTACATCTGTCTCTCTGTGATGGCTCTCTTCTTCCGGCCC 668
 QY TGGCTCATCATGATCTTGTCTTACCTGGCGATCTACCTGATGCGCAACGACGAAACCGC 612
 Db TGCCCTCATCATGGGCTGGTCTTACCGCGCATCTACCGAGTGGCCAAAGCTGGCGACGCGC 728
 QY AGAGGTCCCAAGGCGCAAGGGGGGGCTGGGCGAAGGGTGAATCCAAAGCAAGGCCGACCCGAC 672
 Db A-----CGCTTCAGCGAAGAAAGCGCCGCCCTCGTGGGCCCC 761

| | | | |
|----|------|--|------|
| Db | 762 | GACGGTGGCTCCCGCACTACGAAACGGGCTGGGGCGGCGGCGAGGCGCAGGAAC | 821 |
| Qy | 733 | GAGGTCAACGACACTCCGAGTCTCACTGGGGAGAGAGAGAGGGGAGACCCCTGAAGAT | 792 |
| Db | 822 | GGGCACTGCGGCGCCCCCGCGCGCAGCGTGAAGCCGGAAGAAAGCAGCGCAGGCGCGAG | 881 |
| Qy | 793 | ACTGGAGCCCGGGCCTTGGCAACCGAGTTGGGCTGCCCTTCCCACTCAGGCGCAGGGCCAG | 852 |
| Db | 882 | AGGCGGCGGC-----GCCGGGCGCG | 902 |
| Qy | 853 | AAGAGGGTGTTTTGGGGCATCTCCAGAGATGAAGCTGAAGAGAGAGAGAGAG | 912 |
| Db | 903 | TTCGGCGGGGGCGGGCGGGCGGAGCGGGCGCGGAGGGGGCGCGGGCGGTGGACGGG | 962 |
| Qy | 913 | GAGAGAGAGAAAGATGTGAACCCCAAGGACATGTCAGTGTCTTCGGGCTTCAGTTTCAC | 972 |
| Db | 963 | CAGGGGGCGGCTGAATCGGGGGCGGTGACCGGCTCCAGGATCCCGGGGCGCGGTGGCGCG | 1022 |
| Qy | 973 | CCCCCGCTGACAGCAGCCACAGGGTCCCCGGGGTGTGCGCACCCCTAAGTGGCCAGGTGCTC | 103 |
| Db | 1023 | CTGTGCGGCGGCAAGCTCGCGCTCCCTCGAATTTCTTCTGTGGCGCGCGCGGGCGCGC | 108 |
| Qy | 1033 | CTGGGCAAGGAGCGTGGTGTCTAATAGATGGGACATGGTGAGCGTGAAGGGCGCAGCTAGCC | 109 |
| Db | 1083 | AGCAGC-----GTGTGCGCGCGCAAGGTGGCGCAGGGG | 111 |
| Qy | 1093 | CGGAGGAAGCGTTCACTTCGTGTGCTGTGTGTCATTTGCGTTTTGTCTCTGTGG | 115 |
| Db | 1116 | CGCGAGAAAGCGGTTCACTTTGTGTGGCTGTGTATGAGGTGTGTTCTGTCTCTGTGG | 117 |
| Qy | 1153 | TTCCCGCTTCTTCAAGCTACAGCGCTGGGGCGCATGTGGCCGAAGACATTCGMAAGTGGCC | 121 |
| Db | 1176 | TTCCCGCTTCTTCAAGCTACAGCGCTGTAGCGGCATCTGCGGAGGGCTGGCCAGGTGCC | 123 |
| Qy | 1213 | CATGGCCTCTTCCAGTCTTCTTCTGTGATCGGCTACTGCAACAGCTCACTGAACCTGTTT | 127 |
| Db | 1236 | GCGCGGCTTTCAGTGTCTTCTTCTGTGATCGGCTACTGCAACAGCTCGCTCAACCCGGTTC | 129 |
| Qy | 1273 | ATCTACACATCTTCAACCAAGACTTCGGCGGTGCCTTCCGAGAGATCCTGTGCGCGCG | 133 |
| Db | 1296 | ATCTACAGGCTTCAACCAAGATTTCCGGCGATCCTTTAAGACATCTCTTCCGACGG | 135 |
| Qy | 1333 | TGGA | 1336 |
| Db | 1356 | AGGA | 1359 |

Search completed: February 8, 2004, 01:46:18
Job time : 529.717 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 7, 2004, 20:15:32 / Search time 3132.92 Seconds
(without alignments)
10496.265 Million cell updates/sec

Title: US-09-692-077d-1

Perfect score: 1353
Sequence: 1 atgacaccacagagaccctca.....ggacccagagcgctgtga 1353

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:
1: em_estsda:*
2: em_esthma:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estc:*
11: gb_hic:*
12: gb_estc3:*
13: gb_estc4:*
14: gb_estc5:*
15: em_estfun:*
16: em_estcom:*
17: em_ges_hum:*
18: em_ges_hiv:*
19: em_ges_pln:*
20: em_ges_vrt:*
21: em_ges_fun:*
22: em_ges_mam:*
23: em_ges_mus:*
24: em_ges_pro:*
25: em_ges_rtd:*
26: em_ges_phg:*
27: em_ges_vrt1:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 654.4 | 48.4 | 872 | 29 | ECOA2BAR |
| 2 | 513.2 | 37.9 | 1044 | 13 | BO880026 |
| 3 | 442.4 | 32.7 | 2410 | 11 | BC035047 |
| 4 | 390.6 | 28.9 | 3594 | 11 | AK046802 |

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 5 | 324 | 23.9 | 1201 | 9 | AL544609 |
| 6 | 322.4 | 23.8 | 1201 | 9 | AL530418 |
| 7 | 295.4 | 21.8 | 988 | 13 | BO887729 |
| 8 | 278.4 | 20.6 | 691 | 10 | BB643669 |
| 9 | 278.4 | 20.6 | 2736 | 11 | AK046211 |
| 10 | 267.2 | 19.7 | 909 | 14 | CA477609 |
| 11 | 262.6 | 19.4 | 677 | 28 | B2138792 |
| 12 | 262.2 | 19.5 | 896 | 29 | CNS03BQM |
| 13 | 222.8 | 16.5 | 736 | 13 | BU468891 |
| 14 | 218.4 | 16.1 | 570 | 14 | CD552619 |
| 15 | 218.4 | 16.1 | 855 | 29 | GCRA2MAR |
| 16 | 211 | 15.6 | 966 | 29 | CNS02NV2 |
| 17 | 205.8 | 15.2 | 893 | 12 | BI459381 |
| 18 | 205.4 | 15.2 | 415 | 9 | AW785035 |
| 19 | 198.6 | 14.7 | 805 | 29 | CNS03CEB |
| 20 | 184.4 | 13.6 | 801 | 29 | GCRA2CAR |
| 21 | 183.2 | 13.5 | 863 | 14 | CD361190 |
| 22 | 182.2 | 13.5 | 1201 | 9 | AL573897 |
| 23 | 178.8 | 13.2 | 774 | 29 | AGAA2C2AR |
| 24 | 175.8 | 13.0 | 819 | 29 | CCAA2BAR |
| 25 | 175 | 12.9 | 1176 | 9 | AL549866 |
| 26 | 174.6 | 12.9 | 619 | 10 | AW16723 |
| 27 | 172.8 | 12.8 | 1201 | 9 | AL544577 |
| 28 | 167.6 | 12.4 | 777 | 29 | LRBA2AR |
| 29 | 164.4 | 12.2 | 555 | 9 | AL588968 |
| 30 | 161.8 | 12.0 | 301 | 14 | T39448 |
| 31 | 159.8 | 11.8 | 753 | 29 | SCAA2CAR |
| 32 | 158.8 | 11.7 | 575 | 13 | BU377890 |
| 33 | 158.4 | 11.7 | 767 | 13 | BU376517 |
| 34 | 157.4 | 11.6 | 451 | 9 | AI461341 |
| 35 | 156.6 | 11.6 | 1010 | 29 | CNS04CMQ |
| 36 | 155.6 | 11.5 | 1201 | 9 | AL530417 |
| 37 | 155.4 | 11.5 | 859 | 14 | CD360383 |
| 38 | 155.4 | 11.5 | 920 | 14 | CD360119 |
| 39 | 155.2 | 11.5 | 882 | 29 | H1PA2C2AR |
| 40 | 154.8 | 11.4 | 825 | 29 | ARUA2BAR |
| 41 | 154.6 | 11.4 | 1080 | 29 | CC240340 |
| 42 | 154.4 | 11.4 | 890 | 29 | CNS02MK9 |
| 43 | 153.8 | 11.4 | 911 | 14 | CD360520 |
| 44 | 153.2 | 11.3 | 974 | 29 | PTRA2BAR |
| 45 | 153 | 11.3 | 926 | 29 | CNS012C8 |

ALIGNMENTS

RESULT 1
ECOA2BAR
LOCUS
DEFINITION
Horse alpha2 adrenergic receptor gene fragment probably subtype b,
genomic survey sequence.
ACCESSION
AL606560
VERSION
AL606560.1 GI:15591917
KEYWORDS
GSS; Alpha2 adrenergic receptor gene.
SOURCE
Equus caballus (horse)
ORGANISM
Equus caballus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE
1 (bases 1 to 872)
Hunter, C. and Elgar, G.
TITLE
Alpha2 adrenergic receptor gene
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 872)
Hunter, C.
TITLE
Direct Substition
JOURNAL
Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hmp.mrc.ac.uk
FEATURES
source
1..872
Location/Qualifiers
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| Best Local Similarity | 87.0%; | Pred. No. 2.26-116; | | |
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| DB | 1 | TGCGCCATCAGCTTGGACCGTCACTGGGCGCGGAGCCGCGCGCTGGAGTACCACTTCCAA | 60 | |
| QY | 370 | CGACCCCGCGCGCGCATCAATGTCATCTCTCATCTGTGTGGCTCATTCGCGCGCGTCA | 429 | |
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| QY | 430 | TGCGTGCCTGCGCGCTCATCTTCAAGGGCGACCAAGGGCGCCCGACGCGCGAGCGCCCG | 489 | |
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| QY | 550 | CCTTGCCTCATCATGATCTCTTGTCTTCACTGGCGCATCTATCTGATGCGCAACGACGAC | 609 | |
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| QY | 670 | GACATATGTGGGCTTTTGGCTCATGCGCCAACTGCGACCCCTGGGCTC---TGTGGCTCT | 726 | |
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| QY | 727 | GCCAGAGAGTCAAGGACATCGAAGTCCACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG | 786 | |
| DB | 421 | GCGGAGAGGCGCAATGACACTCGAGCGCCACTGGGAGAG---AGAGGCGAGAGAGAGAG | 477 | |
| QY | 787 | GAGATATCTGGGACCCGAGGCTTGGCCACCTGTTGGCTGCTGCTTCCCAACTCAGGCGAG | 846 | |
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| DB | 538 | GATCAGAGAGAGAGAGATTTGTGGGAGATCTTGGAGAGAGAGAGAGAGAGAGAGAGAA | 597 | |
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| DB | 598 | GAG | 657 | |
| QY | 955 | CCGAGCTTACCTTCAAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | 1014 | |
| DB | 658 | CCGAGCTTACCTTCAAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG | 717 | |
| QY | 1015 | CTAAGTGGCGAGGCTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 1074 | |
| DB | 718 | CTAAGTGGCGAGGCTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 777 | |
| QY | 1075 | CGAAGAGCGCGAGCTTCAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 1134 | |
| DB | 778 | CGGCGGAGCGAGCTTCAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 837 | |
| QY | 1135 | GTTTTGTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG | 1168 | |
| DB | 838 | GTCTTGTGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG | 871 | |
| RESULT 2 | | | | |
| LOCUS | B0880026 | 1044 bp | mRNA | linear |
| DEFINITION | ABENCCUR1_811358 lrpak1 dorsal root ganglion Homo sapiens cDNA | | | |
| | clone IMAGE:6179035 5'...mRNA sequence. | | | |
| | | | | EST 16-AUG-2002 |

[illegible]

| | | | |
|----|------|--|------|
| OY | 824 | CTGCCCTTCCCAACTCAGGCCAGGGCCAGAAAGAGGGGTGTTGTGAGGCATCTCCAGAG | 883 |
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| OY | 884 | ATGAAGCTGAAGAAGAGGAGAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 943 |
| Db | 421 | ATGAAGCTGAAGAAGAGGAGAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG | 472 |
| OY | 944 | TGCCAGTGTCTCCGGCTCAGCTTGACATCCCGCTGCACAGCCACAGGAGCTCC--G | 1001 |
| Db | 473 | TGCCAGTGTCTCCGGCTCAGCTTGACATCCCGCTGCACAGCCACAGGAGCTCCCGG | 532 |
| OY | 1002 | GATGCTGGCAACC--TACGTGGCCAGGTGCTCC--TGAGGACAGGGCCTGGG-TGCTATA | 1056 |
| Db | 533 | GATGCTGGCAACCCTTACCGTAGGCCAGAGTGCTCCCTGGGACAGGGCCGTGGGATGCTATA | 592 |
| OY | 1057 | GATGGGCAAGTGTGCGCTGCG----AAGGGCCGACGTGACCCGGAGGAA | 1100 |
| Db | 593 | AATGGGGAGAGTGTGAGCCGTCACACCGGAGCGAGCTGAACCCGGAGAA | 640 |

| RESULT 3 | BC035047 | LOCUS | DEFINITION |
|----------|----------|-------|---|
| BC035047 | 2410 bp | mRNA | linear |
| | | | HTC 23-SEP-2002 |
| | | | Homo sapiens, similar to adrenergic, alpha-2A-, receptor, clone |
| | | | IMAGE:5266354, mRNA. |

| | | |
|----------|----------------------|-------------|
| VERSION | BC035047.1 | GI:23272892 |
| KEYWORDS | HTC. | |
| SOURCE | Homo sapiens (human) | |
| ORGANISM | Homo sapiens | |

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 2410)
Strausberg, R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian

| REMARK | NIH-MGC Project URL: http://mgc.nci.nih.gov |
|---------|--|
| COMMENT | Contact: MGC help desk |

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shrikant Toehlyuti and Piero Carninci (RIKEN)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
Contact: amadams@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Series: IRAP Plate: 73 Row: 0 Column: 16
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15718669
 This clone has the following problem: frame shifted.

FEATURES
SOURCE

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/clone="IMAGE:526354"
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/clone_1fb="NH MGC_97"
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| Best Local Similarity | 62.8%; | Pred. No. 2.4e-75; | | |
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| QY | 13 | CCCTTACTCCGTGAGGCGCAAGAGGGCCATAGGCGGCGCATCATCTTCTCCATTTCTT | 74 |
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| Db | 411 | GCCCCAAAACCTCTTCTGCTGTGTCTCTGGCTCTCGGCGGAACTCTGTGTGGCACGCTGT | 470 |
| QY | 195 | CATCCCTTTCCTGGGTGGCAAGAGGCTGTGGGCTACTGTGGATCTTCCGGGCAAGGTG | 254 |
| Db | 471 | CATCCCTTCTGCTGGGCAAGAGGATATGGGCTACTGTGGATCTTCCGCAAGGCTTGGT | 530 |
| QY | 255 | CGAGTGTACTTGGCGGCTCGACGTGCTCTTCTGCACTGTGTCAATCGTGTGACCTGTGGCG | 314 |
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| QY | 315 | CATCAGCTTGGACCGGCTACTGTGGCCGTGAGCGCGCGCTGGAGTCAAACTTCAGAGCGCAC | 374 |
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| QY | 435 | GCCGCGCCCTCATCT-----ACAAGGGCGACCAAGGGCCCCCGACGCCGCGCGGCGCCC | 485 |
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 Oy 1146 CTAGTGGTCTCCCTCTCTTCTTCTGAGCTACAGCTGCGGCGCATCTGCGGAGAGAGCTGCA 1205
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 Oy 1206 GGTGCGCCATGCGCTCTTCTGAGCTTCTTCTGAGCTGAGCTGCAAGAGCTGCTGAA 1265
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RESULT 4 AK046802 3594 bp mRNA linear HTC 05-DEC-2002
 LOCUS AK046802
 DEFINITION Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN

full-length enriched library, clone B830011M21 product:ALPHA-2A
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accession AK046802
 version AK046802.1 GI:26091726
 keywords HTC; CAP trapper;
 source Mus musculus (house mouse)
 organism Mus musculus

reference 1 Carninci, P. and Hayashizaki, Y.
 title High-efficiency full-length cDNA cloning
 journal Meth. Enzymol. 303, 19-44 (1999)
 medline 99279253
 pubmed 10349636

reference 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 title Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 genome Res. 10 (10), 1617-1630 (2000)
 journal 20499374
 medline 11042159
 pubmed 11042159

reference 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 title Komno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, D.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 genome Res. 10 (11), 1757-1771 (2000)

journal 20530913
 medline 11076861
 pubmed 11076861

title Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Arakawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, J., Fukuda, S.,
 Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, W., Gaasterland, Y., Gissi, C., King, B., Kochiwa, H.,
 Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,

Quackenbush, J., Schriml, L.M., Staab, F., Suzuki, R., Tomita, M.,
 Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
 Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
 Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
 Fletcher, C., Fujita, M., Gariboldi, M., Guelinrich, S., Hill, D.,
 Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
 Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
 Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,
 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohse, S.,
 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)

title 5 The PANTOM Consortium and the RIKEN Genome Exploration Research
 group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

reference 6 (bases 1 to 3594)
 title Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Konda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murate, M.,
 Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M., and Hayashizaki, Y.
 direct Submission

title Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 comment CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse libraries.
 please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/.
 location/Qualifiers

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| OY | 726 | TGCCAGAGAGTCAACGAGCACTCGAAGTCACTGGGGAGAAAGAGAGGGGGAGACCC | 785 |
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| OY | 846 | GGGCGAGAAAGAGGTGTTGTGGGGGCACTTCAGAGAGATGAAGCTGAAGAGAGAGAGA | 905 |
| Db | 1760 | -----GTTCGTGCTCGAGAGACGCCAGCGGCCCCCGGGGGCCCCGACACCC | 1806 |
| OY | 906 | GGAAGAGAGAGAGAGAAAGTGTGAACCCCAAGGCAGTGCAGTGTCTCGGCTCAGC | 965 |
| Db | 1807 | GACGCGGCGCCCCCGAGCCAAAGGGCAACCCGSGGAGTCAAGTGAACCGGGGGAGACAGT | 1866 |
| OY | 966 | TTGCAAGCCCCCGCTGCGAGAGCCACAGGGCTCCCGGGTGTGTGGCAACCTCACTGTGGCA | 1025 |
| Db | 1867 | CTGCGCGCGGCGCGGCGCGCGGGCGCGGGGGCTTC----- | 1907 |

| | | | |
|----|------|---|------|
| Qy | 1026 | GGTCTCTTGGGACAGGGGCGTGGGTGCTATATGATGGGACAGTGGTGGCGTCCAAAGGGCGCA | 1085 |
| Db | 1308 | GGGGTCCGGGACAGGAAGAGGCGGGCGGGGGCGCCAAAGCTTCGGGCTGGCCGGGAG | 1967 |
| Qy | 1086 | GCTGACCCCGGAGAGAGCGCTTACCTTTCGTGCTGTGTGCTATATGAGCGCTTTTGTGCT | 1145 |
| Db | 1968 | GCAAACACGGGAGAAACGCTTCAAGTTCTGTGCTGGCGGTGGTGAATCGGCGGTTCGTGTGT | 2027 |
| Qy | 1146 | CTGCTGGTTCCTCTTCTTTCAGCTACAGCTTGGGCGCATCTGCCGGAAGCACTGCA | 1205 |
| Db | 2028 | GTGTGGTTTCCGTTCTTTTTCACCTTACAGCTATAGCGGTGG-----CTGCC | 2078 |
| Qy | 1206 | GGTCCCCCAATGCTCTTCCAGTCTTCTTCTGATGGGCTACTGCAACAGCTCACTGAA | 1265 |
| Db | 2079 | GGTCCCCAGCGCTCTTCAACTCTTCTTCTGTGGTTCGGCTACTGCAACAGCTGCTGAA | 2138 |
| Qy | 1266 | CCCTGTAATCAACCAATCTTCAACCAAGACTTCCGCGGCTTCCGGAGGATCTGTG | 1325 |
| Db | 2139 | CCCTGTAATCAACCAATCTTCAACCAAGACTTCCGCGGCTTCAAGAGATCTCTGTG | 2198 |
| Qy | 1326 | CCG | 1328 |
| Db | 2199 | CCG | 2201 |

| | |
|------------|--|
| RESULT 5 | |
| AL544609 | |
| LOCUS | |
| DEFINITION | AL544609 1201 bp mRNA linear EST 31-MAY-2003 |
| ACCESSION | AL544609 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA |
| VERSION | clone CSOD1021YC24 5-PRIME, mRNA sequence. |
| KEYWORDS | AL544609 |
| SOURCE | AL544609.2 GI:31266452 |
| ORGANISM | EST. |
| | Homo sapiens (human) |
| | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |
| TITLE | 1 (bases 1 to 1201) |
| JOURNAL | Li, W. B., Gruber, C., Jesse, J. and Polayes, D. |
| COMMENT | Full-length cDNA libraries and normalization |
| | Unpublished |
| | On Feb 15, 2001 this sequence version replaced gi:12877089. |
| | Contact: Genoscope |
| | Genoscope - Centre National de Sequencage |
| | Bp 191 91006 EVRY cedex - France |
| | Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr |
| | Library was constructed by Life Technologies, a division of |
| | Invitrogen. This sequence belongs to sequence cluster 5594.f For |
| | more information about this cluster, see |
| | http://www.genoscope.cns.fr/ |
| | cg1-bin/cluster.cgi?seq=CSOD1021BBI20P1&cluster=5594.f. Contact : |
| | Feng Liang Email : fliang@lifetech.com URL : |
| | http://fulllength.invitrogen.com/InvitrogenCorporation 1600 |
| | Barclay Avenue genoscope sequence ID : CSOD1021BBI20P1. |

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FEATURES
SOURCE
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            /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
            /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
        155 a 430 c 425 g 184 t 7 others
BASE COUNT
ORIGIN

```

| | | | | |
|---------------------------|-------|--------------------|-----------|--------------|
| Query Match | 23.9% | Score 324; | DB 9; | Length 1201; |
| Best Local Similarity | 74.8% | Pred. No. 1.5e-52; | | |
| Matches 446; Conservative | 0; | Mismatches 145; | Indels 5; | Gaps 3; |

RESULT 7
 BQ887729 988 bp mRNA linear EST 16-AUG-2002
 LOCUS BQ887729
 DEFINITION AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
 5', mRNA sequence.
 ACCESSION BQ887729
 VERSION BQ887729.1 GI:22279743
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 988)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@ds-r@mail.nih.gov
 Tissue Procurement: Susan L. Sullivan, PhD.
 CDNA Library Preparation: Reggen, Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13739 row: m column: 06
 High quality sequence start: 8
 High quality sequence stop: 509.
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 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:6313133"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_129"
 /note="Organ: olfactory epithelium; Vector:
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 unidirectionally. Primer: Oligo dT. Average insert size
 2.2 Kb. Constructed by Reggen, Invitrogen Corp. Note: this
 is a NIH MGC Library."
 18 a NIH_MGC Library."
 BASE COUNT 158 a 349 c 300 g 181 t

Query Match 21.8%; Score 295.4; DB 13; Length 988;
 Best Local Similarity 76.4%; Pred. No. 4.9e-47;
 Matches 389; Conservative 0; Mismatches 116; Indels 4; Gaps 2;

106 GCTGTGTGACGACCGCTGCTGCGCGCCCTCAGAACTGTTCCGTGCTGCTGCGC 165
 19 GCTGTGTGACGACCGCTGCTGCGCGCCCTCAGAACTGTTCCGTGCTGCTGCGC 78
 166 GCCGC-CGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 224
 79 TCAGTACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 138
 225 GGGCTACTGTAATCTCCGGCGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
 139 GGGCTACTGTAATCTCCGGCGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 198
 285 CTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 344
 199 CTGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 258
 345 CCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 404
 259 GCAAGGGTGAATCACTGAAGGCGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCT 318
 405 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
 319 CGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 375
 465 CCCCAGCG 524

Db 376 GCCCGACGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
 525 CTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 584
 Db 436 CTCCTGATGAGGCTCTCTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
 585 CTACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
 Db 496 CTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 524

RESULT 8
 BB643669/c 691 bp mRNA linear EST 26-OCT-2001
 LOCUS BB643669
 DEFINITION BB643669 RIKEN full-length enriched, adult male corpora
 quadrigenina Mus musculus cDNA clone B230352011 5', mRNA sequence.
 ACCESSION BB643669
 VERSION BB643669.1 GI:16478370
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 691)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,
 Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda,
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Sasaki,
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,
 D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
 Tsurumatsu, M., and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 JOURNAL Unpublished
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,
 M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Matsubara, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura,
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10
 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,
 Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa,
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, D., Shibata, K., and
 Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.
 Location/Qualifiers
 1..691
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"

[illegible]

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| Matches 388 | Conservative | 0 | Mismatches 151 | Indels 9 |
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| Db | 549 | CCCTTACTCCGTGACGATGACACTGACCGTGGTTTGCTTGCGTGGCTGTCATCTGTT | 490 | |
| QY | 75 | TACCATCTTGGCCAAACGCTCTGTGTATCTGTGCTGTGTGACCAAGCCCTGCTGGCGC | 134 | |
| Db | 489 | CACACTATTGGCAACGTCGTGTATTATCCGGGTGTTCAACAGTCCGCGCTCAAGC | 430 | |
| QY | 135 | CCCTGAGAACCGTTCTGTGTGCTGTGCTGAGCCGCGCCGACATCTGTGTGGCCACGCTAT | 194 | |
| Db | 429 | TCCCAAAACCTCTTCTGTGTGTCTCTGTGTCTCTGTGCTCAGCGGACATCTGTGTGGCAACGCTGTGT | 370 | |
| QY | 195 | CATCCCTTCTGCTGAGCCAAAGAGCTGTGGGCTACTGTGTACTTCCGCGCAACGTGTG | 254 | |
| Db | 369 | CATTCCCTTCTTCTTGGCCAAAGAGTTATGGGTACTGTGTACTTGTGTAAGTGTGTG | 310 | |
| QY | 255 | CGAGGTGTAACGTGGGCTTCGANTGTCTCTTCTGACCTCTGTCCATCTGTGCACCTGTGGC | 314 | |
| Db | 309 | TGAGATCTATTGTGGTCTTCGAGTGTCTCTTTTGGCAAGTGTCCAAATGACACTGTGTGGC | 250 | |
| QY | 315 | CATGACGCTGGACCGCTACTGGGCGGTGAGCCGCGCTGAGATCACTCAACCGGAC | 374 | |
| Db | 249 | CATGACGCTTGAACCGCTACTGTGTTCATACAGAGGCCATCGAGTCAACCTGMAAGCGAC | 190 | |
| QY | 375 | CCCGGCGCGCATCAAGTGCATCATCTCACTGTGTGTGCTCATCGCGCGGTATCTCGCT | 434 | |
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| Db | 129 | CCCGGCACTCATCTCATAGAGAAAGGCGCTGCGCGCGGCGGACGCGCGGAGCC | 70 | |
| QY | 486 | CCAGTGAAGCTCAACGAGAGCGCTGTGTATCTGTGGCTCCAGACTCGATCTTCTTCTT | 545 | |
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| Db | 9 | GCGGCTT 2 | | |

| LOCUS | AK046211/c |
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| DEFINITION | 2736 bp mRNA linear HTC 05-DEC-2002 |
| ACCESSION | AK046211 |
| VERSION | Mus musculus adult male corpora quadrigemina cDNA, RIKEN |
| KEYWORDS | full-length enriched library, clone: B23532011 Product: unknown EST, full insert sequence. |
| SOURCE | AK046211 |
| ORGANISM | AK046211.1 GI:26091387 |
| REFERENCE | HTC; CAP trapper. |
| REFERENCE | Mus musculus (house mouse) |
| REFERENCE | Mus musculus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| REFERENCE | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| REFERENCE | 1 Carninci, P. and Hayashizaki, Y. |
| REFERENCE | High-efficiency full-length cDNA cloning |
| REFERENCE | Meth. Enzymol. 303, 19-44 (1999) |
| REFERENCE | 99279253 |
| REFERENCE | 10349636 |
| REFERENCE | 2 |
| REFERENCE | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., |
| REFERENCE | Itoh, M., Komo, H., Okaaki, Y., Muramatsu, M., and Hayashizaki, Y. |
| REFERENCE | Normalization and subtraction of cap-trapper-selected cDNAs to |
| REFERENCE | prepare full-length cDNA libraries for rapid discovery of new genes |
| REFERENCE | Genome Res. 10 (10), 1617-1630 (2000) |
| REFERENCE | 11042159 |
| REFERENCE | 20499374 |
| REFERENCE | Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., |
| REFERENCE | Waki, Y., Kikuchi, T., Maehara, H., Itoh, M. |

| | |
|-----------|--|
| TITLE | Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Onara, E., Matsubiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. |
| JOURNAL | RIKEN Integrated sequence analysis (RISA) system--384-format |
| MEDLINE | sequencing pipeline with 384 multicapillary sequencer |
| PUBMED | Genome Res. 10 (11), 1757-1771 (2000) |
| REFERENCE | 20530913 |
| AUTHORS | 11076861 |
| TITLE | 4 |
| JOURNAL | Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., |
| MEDLINE | Arkawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., |
| PUBMED | Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., |
| REFERENCE | Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., |
| AUTHORS | Kadote, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., |
| | Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., |
| | Kuehl, P., Lewis, S., Matsuno, Y., Nikaido, I., Peeble, G., |
| | Quackenbush, J., Schiraldi, L.M., Steubli, F., Suzuki, R., Tomita, M., |
| | Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., |
| | Baldarelli, R., Barah, G., Blake, Y., Boffelli, D., Bojunga, N., |
| | Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., |
| | Fletcher, C., Fujita, M., Gariboldi, M., Gustcinich, S., Hill, D., |
| | Hotamoni, H., Hume, D.A., Kamlyu, M., Lee, N.H., Lyons, P., |
| | Macchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., |
| | Ring, B., Rongwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., |
| | Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., |
| | Toyokaka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilmberg, L., |
| | Wyshak-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S., |
| | Hayashizaki, Y. |
| TITLE | Functional annotation of a full-length mouse cDNA collection |
| JOURNAL | Nature 409 (6821), 685-690 (2001) |
| MEDLINE | 21085660 |
| PUBMED | 11217851 |
| REFERENCE | 5 |
| AUTHORS | The FANTOM Consortium and the RIKEN Genome Exploration Research |
| TITLE | Group Phase I & II Team. |
| JOURNAL | Analysis of the mouse transcriptome based on functional annotation |
| MEDLINE | of 60,770 full-length cDNAs |
| PUBMED | Nature 420, 563-573 (2002) |
| REFERENCE | 6 (bases 1 to 2736) |
| AUTHORS | Adachi, J., Aizawa, K., Akimura, T., Aikawa, T., Bono, H., Carninci, P., |
| | Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., |
| | Fukuda, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., |
| | Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., |

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

FEATURES

source

1. 2736
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/strain="C57BL/6J"
/db_xref="FANTOM:DB:B230352011"
/db_xref="taxon:10090"
/clone="B230352011"
/sex="male"
/tissue_type="corpora quadrigemina"
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/dev_stage="adult"
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BASE COUNT 557 a 747 c 904 g 528 t
ORIGIN

Query Match 20.6%; Score 278.4; DB 11; Length 2736;
Best Local Similarity 70.8%; Pred. No. 1.2e-43;

Matches 388; Conservative 0; Mismatches 151; Indels 9; Gaps 1;

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Db 249 CATCAGCTGAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
QY 375 CCGCGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424

Db 189 GCCGCTGCATCAGAGCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 130
QY 435 GCCGCTGCATCT-----ACAAGGCGCAGCAGGCGCCCGCAGCGCGCGCGCC 485
Db 129 CCGGCACTCATCTTCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 70
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Db 69 AAGCTCAAGATCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 10

QY 546 TGCTCTCT 553
Db 9 CCGGCTT 2

RESULT 10

CA477609

LOCUS CA477609 909 bp mRNA linear EST 12-NOV-2002
DEFINITION AGENCOURT 10671423 NCI CGAP Zemb3 Danio rerio cDNA clone
IMAGE:6801483 5', mRNA sequence.

ACCESSION

CA477609 GI:24933961

VERSION

CA477609.1 GI:24933961

KEYWORDS

EST.
Danio rerio (zebrafish)
Danio rerio

SOURCE

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
Cyprinidae; Danio.

REFERENCE

1 (bases 1 to 909)
NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

Unpublished
National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished
Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapds-remail.nih.gov
Tissue Procurement: Dr. Chi-Bin Chien
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M14321 row: e column: 02
High quality sequence start: 17
High quality sequence stop: 644.

Location/Qualifiers

FEATURES

source

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/lab_host="DH10B (T1-resistant)"
/clone_lib="NCI CGAP Zemb3"
/note="Vector: pCMV-SPORT6.cdb; Site 1: EcoRV; Site 2:
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insert size 2.1 kb. Constructed by J. Wang (Research
Genetics, Invitrogen Corp) from tissue donated by L. Zon
(Harvard University). Note: this is a NCI CGAP Library."

BASE COUNT 156 a 287 c 266 g 200 t
ORIGIN

Query Match 19.7%; Score 267.2; DB 14; Length 909;
Best Local Similarity 76.2%; Pred. No. 1.3e-41;

Matches 329; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

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QY 76 ACCATCTTGGCAAGCTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 135
Db 366 ACTATGCTGGAAATGTTCTTGATGCTGCGGCTTTGACAGCGCGCGCTGCGGCT 425

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| Oy | 136 | CCTAGAAACCGTTCCTGATGTCGTCGGCCGCGCCGACATTCCTGGTGGCAGCCTATC | 195 |
| Db | 426 | CCACGAACCTCTTCTGTGTGTCGTCGCCGCGGACATATGTGTGGCACCGCTGTG | 485 |
| Oy | 196 | ATCCCTTCTGCTGGCCAAAGAGCTGCTGGGCTACTGTGTACTTCCGGCGACGCTGTGC | 255 |
| Db | 486 | ATCCCGTTCCTCCTGCGACAGAGATCATGGGATATCTGTGTACTTCCGAGACCTGGTGC | 545 |
| Oy | 256 | GAGGTGATCCTGGCGCTGACGTGCTCTTCTGACCTTCGTCAATGTGTCACCTGTGGCC | 315 |
| Db | 546 | GCGTTTACCTGGCCCTGGATGTGTGCTTGTGACAGTCTCATGTGTCACCTGTGGCC | 605 |
| Oy | 316 | ATCAGCTGGAACCGCTACTGGGCGCTGAGCCGCGCGCTGAGTGAATCCAAAGGACAC | 375 |
| Db | 606 | ATCAGCTTGGACAAGGTACTGTGCTCGCTACCAAAAGGGTGGCGCTAACTGAAGGACGG | 665 |
| Oy | 376 | CCGGCGCGCATCAATGTCATCATCTCACTGTGGGCTCATCGCCGCGCTATCTCGTGTG | 435 |
| Db | 666 | CCGAGCGCCCATGAAGTCATGATCCGGGGGGTGTGGCTGATCTCCGCCGTATCTCTTC | 725 |
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| Db | 726 | CTCCGCTCATC | 737 |

| RESULT 11 | 677 bp | DNA | linear | GSS 11-OCT-2002 |
|------------|-----------------|---------------------|-------------------|-----------------|
| B2138792/c | | | | |
| LOCUS | | | | |
| DEFINITION | B2138792 | | | |
| | CH230-256D20.TV | CHORI-230 Segment 2 | Rattus norvegicus | genomic clone |
| | CH230-256D20, | genomic | Burley | sequence. |

| | | |
|-----------|-------------------|--------------|
| ACCESSION | BZ138792 | GI:23779739 |
| VERSION | BZ138792.1 | |
| KEYWORDS | GSS. | |
| SOURCE | Rattus norvegicus | (Norway rat) |
| ORGANISM | Rattus norvegicus | |

| REFERENCE AUTHORS | 1 (bases 1 to 677) | Shatsman, S., Tsengaye, G., Geer, K., Shvartsbeyn Zhao, S., Shetty, J., |
|---|--------------------|--|
| Eukaryota; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. | | |

| | |
|---------|--|
| TITLE | A., Gelberg, E., Overton, L., Russell, D., Chen, D., Riggs, F., de |
| JOURNAL | Jong, P. and Fraser, C.M. |
| COMMENT | Rat BAC End Sequences from Library CHORI-230 MboI segment |
| | Unpublished |
| | Other_GSSs: CH230-256D20.TU |

Contact: Shanying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208

FEATURES
 source
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library
 availability, please contact Peter de Jong (pdejong@mail.cho.org)
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or_eting/information.htm). BAC end
 pages: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Place: 256 row: D column: 20
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 Class: BAC ends.
 Location/Qualifiers
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CHORI-230 Rat (BN/SSNhd/MCw) BAC library produced by

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| BASE COUNT | Pleier de Jong | | |
|------------|----------------|-----|-------|
| ORIGIN | a | c | |
| | 139 | 200 | 220 g |
| | | | 118 c |

| | | | | |
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| Query Match | 19.4% | Score 262.6; | DB 28; | Length 677; |
| Best Local Similarity | 74.4% | Prod. No. 9.7e-41; | | |
| Matches 331; Conservative | 0; | Mismatches 114; | Indels 0; | Gaps 0; |

23 CCGTCAGGCCACAGCGCCATAGCGCGGCATCACCTTCCTCATTTCTTACCATCT 82

Db 502 CCTGCAGGTGACGCTGACGCTGTTGTCCTGAGCTGGCTGCTCATGCTGTTACCCGTGT 443

83 TCGCAACGCTCTGGTCATCCTGGCTGTGTGAACACGCGCTCGGTGGCGCCCCCTCAGA 142

Db 442 TTGGCACTGCTGGTTATTATTCGACAGTGTACACGACCGCGCGCTCAAGCCCCCAAGA 383

143 ACCGTTTCCTGGTCCGCGCCGCGAGATCTCGTGGCACGCTCATATATCCCT 202
 203 TTTGTTTCT 323
 324 TTTGTTTCT

| | | | | |
|-----|-------------------------------------|--------------------------------------|----------------------------------|-----|
| 203 | TTCTGCGTGGGCGGCAACGAGCGTGGAGGAGCGTA | CTTGGCA | CTTTCCGGCGCGACGTCGAGCGAGGCGT | 262 |
| DB | 382 | ATCCATCCTCGAGTGTCTCTGGCTTCAGCGGACATC | CCCGTGGCCACGCGTGGCACTGCGATCCCGCA | 223 |

Db 322 TTTCTTTGGCCACGAGGTATATGGGCTACTGTACTTTGGTAAAGGTGTGGTGGAGACTT 263

263 ACCGTGGCGCTCGACGTCCTTTCTGCACCTCGTCCATCGTGCACTGTGCGCCATCAGCC 322

Db 262 ACTTGCCCTCGACGTCTTTTGACGTTGCCATGAGTGCCTCTGGCGCATCACCC 203

323 TGGACCGCTACTGGGCGCGTGAGCCGCGCGCTGGAGTCAACTTCAGGCGCAACCCCGCGCC 382

Db 202 TTGACCGCTACTGGTTCATCAGCAGGCCATCGAGTACAACCTGAAGCGCAGCCCGGGC 143

383 GCATCAAGTCATCATCTCACTGTGTGGCTATCGCCGCCGTCATTCGCTGCCGCC 442

Db 142 GCATCAAGGCCATTCATTGTCACTGTGTGGGTCACTCTGGGCCGTCACTCTCCCTTCCGGCAC 83

443 TCATCTACAGGGCGACCGAGGGCCC 467

Db 82 TCATCTCATAGAGAAGAGCGCG 58

RESULT 12

| LOCUS | 896 bp | DNA | linear | GSS 01-SEP-2000 |
|------------|---|-----|--------|-----------------|
| CNS03BQW | | | | |
| DEFINITION | Tetradon niaroviridis genome survey sequence PUC-Ori end of clone | | | |

012P03 of Library G from *Tetradodon nigroviridis*, genomic survey sequence.

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| ACCESSION | AL236849 | GI:7895984 |
| VERSION | AL236849.1 | |

KEYWORDS GSS; genome survey sequence.
SOURCE *Tetradodon nigroviridis*

ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorphia; Acanthopterygii; Petromorpha; Tetraodontiformes; Tetraodontidae; Tetraodonti; Tetraodon.

REFERENCE

1
Roest Crollius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quelier, F., Saurin, W. and Weissenbach, J.

| TITLE | Abstract | Keywords | MeSH | Indexing | References |
|---|----------|----------|------|----------|------------|
| Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence | | | | | |

Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL
20296633
MEDLINE
.....

| | |
|---|---|
| <p> PUBMED 10835645 REFERENCE 2 </p> | <p> Tallon C, Davyda C, Ozouf-Costaz C, Bozec Grollius H </p> |
|---|---|

ROBERT COLLINGS, H., DARRISON, O., DARRISON, C., ZUCKER, C. C.,
FIZAMES, C., FISCHER, C., BOUNEAU, L., BILLAULT, A., QUETTER, F.,
SAURIN W., BERNOT A. and WEISSENBACK, J.

| TITLE | Author | Journal | Year |
|---|------------------|---------|------|
| Characterization and repeat analysis of the compact genome of the freshwater pufferfish <i>Tetraodon lineatus</i> | Wang, J., et al. | Nature | 2003 |

JOURNAL
Genome Res. 10 (7), 939-949 (2000)
MEDLINE
20359837

PUBMED 10899143
REFERENCE 3 (bases 1 to 896)
GENOSCOPE.
AUTHORS
TITLE
JOURNAL
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 101 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.

COMMENT

FEATURES
source
1. .896
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Best Local Similarity 73.8%; Pred. No. 4.2e-33;
Matches 282; Conservative 1; Mismatches 99; Indels 0; Gaps 0;

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QY 69 TCTCTTACCATCTTGGGCAACGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 128
DB 548 CTTCTTACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 607
QY 129 GCGCGCCCTCAGAACCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 188
DB 608 CAGAGGCGCGCAGAACCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 667
QY 189 GCTCATCATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248
DB 668 CTTGCTGATGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
QY 249 GTGCTGAGAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 308
DB 728 CTGTGTGGGATTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 787
QY 309 GTGCGCATCAGCTGAGCCGCTACTGAGCCGCTGAGCCGCTGAGAGTCAACTCCAA 368
DB 788 GTGCGCAATAGCTTGGACCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 847
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DB 848 GAGACCCCTCAGCGCGTMAAG 869

RESULT 13
LOCUS BU468891 736 bp mRNA linear EST 30-NOV-2002
DEFINITION 603355259F1 CSEORBN21 Gallus gallus cDNA clone CHEST263e16 5', mRNA
sequence.
ACCESSION BU468891
VERSION BU468891.1 GI:25962468
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 736)
Boardman, P. B., Sans-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,
Fong, M. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 2233534
PUBMED 12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
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constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

BASE COUNT 150 a 214 c 192 g 180 t

ORIGIN
Query Match 16.5%; Score 222.8; DB 13; Length 736;
Best Local Similarity 71.8%; Pred. No. 4.8e-33;
Matches 306; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

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QY 428 TCTGTGCGCGCCCTCATCTCAAGGCGACGAGGCGCCCGCGCGCGCGCGCGCGCG 487
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DB 361 CACCTGCTCATCATGATGCTGTGCTATATATCGATCTACCGGTGCGCAACGATGAAG 420
QY 608 ACCGCA 613

Db 182 TCCTGGGTCAATCTGGCCGTCATCTCCCGCGCTCATCTCCATAGAGAGAGA 241
Qy 464 | GCGCCAGCCG-----CGGGGGGCCCCCAGTGCAGCTCAACAGAGAGCGCTGTACA 517
Db 242 GTGGGACAGGTGAGACCAAGTGGCGGCGAGATGCAGATCAATGACGAGAGTGTACA 301
Qy 518 TCCTGGCCTTCAGCATCGAATCTTTCTTTGCTCTGCTCATCATGATCTGTCTACC 577
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Qy 578 TCGCATCTTACCTGATGCCAAGCGCAGCAACCG 611
Db 362 TCGCATCTTACGATAGCCAGAGGCGAACCAG 395

Search completed: February 8, 2004, 01:25:36
Job time : 3142.92 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 23:41:33 ; Search time 5086.47 seconds

(without alignments)
10809.568 Million cell updates/sec

Title: US-09-692-077D-2

Perfect score: 1344

Sequence: 1 atgagaccaccagagaccctca.....ggaccagagagcgctgtga 1344

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size: 30

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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7: gb_ph:*
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9: gb_pr:*
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12: gb_sy:*
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32: em_htg_other:*
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37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 1242 | 92.4 | 22842 | 9 | AC092603 | AC092603 Homo sapi |
| 4 | 902 | 67.1 | 1353 | 6 | AX350489 | AX350489 Sequence |
| 5 | 902 | 67.1 | 2072 | 6 | AR270618 | AR270618 Sequence |
| 6 | 902 | 67.1 | 2072 | 6 | HUMADRA2RA | M34041 Human alpha |
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| 10 | 558 | 41.5 | 828 | 10 | S67316 | S67316 alpha 2-adr |
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| 13 | 158 | 11.8 | 1194 | 4 | SC1315936 | AJ315936 Sorex cin |
| 14 | 143 | 10.6 | 246 | 10 | S6731782 | S6731782 alpha 2-adr |
| 15 | 137 | 10.2 | 1150 | 4 | CSP251181 | AJ251181 Cynopetru |
| 16 | 127 | 9.4 | 1149 | 4 | AF337539 | AF337539 Pteropus |
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| 18 | 116 | 8.6 | 1168 | 4 | TTA251187 | AJ251187 Typha be |
| 19 | 110 | 8.2 | 1172 | 10 | ARU427256 | AJ427256 Apidontci |
| 20 | 109 | 8.1 | 130 | 10 | S6731781 | S6731781 alpha 2-adr |
| 21 | 107 | 8.0 | 1176 | 10 | SVU315942 | AJ315942 Scitrus v |
| 22 | 101 | 7.5 | 1149 | 4 | CUN427371 | AJ427371 Cabassous |
| 23 | 101 | 7.5 | 1162 | 4 | FCA251174 | AJ251174 Felis cat |
| 24 | 98 | 7.3 | 1165 | 4 | DRI251184 | AJ251184 Dicros b |
| 25 | 97 | 7.2 | 1174 | 4 | ERA2ABREC | Y12521 Erinaceus e |
| 26 | 95 | 7.1 | 1156 | 4 | MLA251107 | AJ251107 Micropota |
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| 30 | 90 | 6.7 | 1177 | 4 | BPH251175 | AJ251175 Balaenopt |
| 31 | 89 | 6.6 | 1179 | 10 | DNI427257 | AJ427257 Dryomys n |
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| 33 | 87 | 6.5 | 1176 | 4 | LAL315940 | AJ315940 Lagenorhy |
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ALIGNMENTS

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| KEYWORDS | | SOURCE | | ORGANISM | | | | |
| | | | | | | | | |
| REFERENCE | | | | | | | | |
| AUTHORS | | | | | | | | |
| TITLE | | | | | | | | |
| JOURNAL | | | | | | | | |

Pred. No. is the number of results predicted by chance to have a

Liggett, Stephen B. (US) ; Small, Kersten M. (US)
Location/Qualifiers
1 1344

| | | | | |
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| ORIGIN | | | | |

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| OY | 121 | CGCTGCTGCGGGCCCTCAGAACCTGTTCCTGAGTGTGCTGAGCGCGCGCCGACATCTTG | 180 |
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| OY | 361 | AATCCAAAGCGACCCCGCGCCGACATCAAGTGATGATCTCTACCTGTGTGCTCATCGCC | 420 |
| Db | 361 | AATCCAAAGCGACCCCGCGCCGACATCAAGTGATGATCTCTACCTGTGTGCTCATCGCC | 420 |
| OY | 421 | GGCGTCAATGTGGTGGCGGCGCTCATCTACAGAGGCGACACAGGCGCCCAAGCGCGGG | 480 |
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| OY | 661 | CCCCGACCCGACCAATGTGTGGGCTTTGGCTCTCAGCAAACTGCAAGCCCTGTGCTGTG | 720 |
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| OY | 781 | ACCCCTGAAGATCTGTGGACCTGGGCTTGTGCCAACCAAGTTGGGCTGCCCTTCCAACTCA | 840 |
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[illegible]

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| MEDLINE | | | | | |
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| AUTHORS | | | | | |
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ACCESSION AC092603.2 GI:16303539
VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 22842)
AUTHORS Martinka,S., Abbot,A., Hawkins,M., Elliott,G. and Doeber,A.
TITLES The sequence of Homo sapiens BAC clone RP11-13906
JOURNAL Unpublished (2001)
AUTHORS 3 (bases 1 to 22842)
REFERENCE Waterston,R.H.
JOURNAL Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 22842)

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AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 22842)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 22842)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916188.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center Project name: H_NH0139J06
Drafting Center: WIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPEC11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanesse, J.J., and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-401C3, 2000 bp overlap; the clone sequenced to the right is RP11-574O17, 2000 bp overlap. Actual end of this clone is at base position 48999 of RP11-574O17.

Polymorphisms have been identified between AC013272 and AC092603.

FEATURES
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ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
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ORGANISM Homo sapiens
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REFERENCE
1 Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patient: WO 0179561-A 1.25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
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VERSION AR270618.1 GI:29701852
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1181 31-Dec-2002;
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACACACAGGAGCCCTACTCTCCGTCAGGCGCAACAGCGGCGCATAGCGGCGGCATCAC 60
Db 413 ATGACACACAGGAGCCCTACTCTCCGTCAGGCGCAACAGCGGCGCATAGCGGCGGCATCAC 472
QY 61 TTCCTCATCTCTTTTACCATCTTTCGCAACGCTCTGATCATCTCGGCTGTGTGACACAGC 120
Db 473 TTCCTCATCTCTTTTACCATCTTTCGCAACGCTCTGATCATCTCGGCTGTGTGACACAGC 532
QY 121 CCTCGCTGCGGCGCCCTCAGAACCTGTTCTGCTGTGCTGAGCGCGCGCATATCTTC 180
Db 533 CCTCGCTGCGGCGCCCTCAGAACCTGTTCTGCTGTGCTGAGCGCGCGCATATCTTC 592
QY 181 GTGGCCAGGCTCATCTCTCTCTGTCGCAACAGAGTGTGGCTGCTACTGTATCTTC 240
Db 593 GTGGCCAGGCTCATCTCTCTCTGTCGCAACAGAGTGTGGCTGCTACTGTATCTTC 240
QY 241 CGGCGCAGGCTGTCGAGAGTACCTGCTGCTGCAAGCTGCTCTTGTGCACTTGTCTATC 300
Db 653 CGGCGCAGGCTGTCGAGAGTACCTGCTGCTGCAAGCTGCTCTTGTGCACTTGTCTATC 360
QY 301 GTGCACTGTGCGGCATCAGCTGAGCGGCTGACCTGAGCGGCGCTGAGAC 420
Db 713 GTGCACTGTGCGGCATCAGCTGAGCGGCTGACCTGAGCGGCGCTGAGAC 472
QY 361 AACTCCAAAGGCAACCCGCGCGCGATCAAGTGCATCTCTGATGTGTGCTCATCGCC 480
Db 773 AACTCCAAAGGCAACCCGCGCGCGATCAAGTGCATCTCTGATGTGTGCTCATCGCC 832
QY 421 GCGCTCATCTGCTGCGCGCCCTCATCTCAAGAGGCGCAAGGCGCCCAAGCGCGCGG 480
Db 833 GCGCTCATCTGCTGCGCGCCCTCATCTCAAGAGGCGCAAGGCGCCCAAGCGCGCGG 892
QY 481 CGGCGCAGGTCAGGTCACCAAGAGGCTGTGATCTGCTGAGGAGAGAGAGAGAGAG 900
Db 893 CGGCGCAGGTCAGGTCACCAAGAGGCTGTGATCTGCTGAGGAGAGAGAGAGAGAG 952
QY 541 TTCTTTGCTCTTGTGCTCATCTGATCTCTGCTCAAGGCTGCTGATCTGATGCGCAA 600
Db 953 TTCTTTGCTCTTGTGCTCATCTGATCTCTGCTCAAGGCTGCTGATCTGATGCGCAA 1012
QY 601 CGAGGCAACCGCAAGGTCCTCAAGGCGCGGCTGAGGAGGCTGAGTCAAGCAG 660
Db 1013 CGAGGCAACCGCAAGGTCCTCAAGGCGCGGCTGAGGAGGCTGAGTCAAGCAG 1072
QY 661 CCCGACCCGACCATGTCGAGGCTTTTGGCTCAAGCAATCTGAGCTGCTGTG 720
Db 1073 CCCGACCCGACCATGTCGAGGCTTTTGGCTCAAGCAATCTGAGCTGCTGTG 1132
QY 721 GCTTCTGCAAGAGTCAAGCACTCGAAGTCACTGAGGAGAGAGAGAGAGAGAGAG 780
Db 1133 GCTTCTGCAAGAGTCAAGCACTCGAAGTCACTGAGGAGAGAGAGAGAGAGAGAG 1192
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QY 841 GGCACGGGCGAGAGAGGGGTGTTGTGGGCGATCTCCAGAGAGATGAAGCTGAAGAGAG 900
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Db 1253 GGCACGGGCGAGAGAGGGGTGTTGTGGGCGATCTCCAGAGAGATGAAGCTGAAGAGAG 1312
QY 901 GA 902
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Db 1313 GA 1314

RESULT 6
HUMADRA2RA 2072 bp DNA linear PRI 30-OCT-1994
LOCUS Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
DEFINITION M34041
ACCESSION M34041.1 GI:178197
VERSION alpha-2-adrenergic receptor; plasma membrane protein;
KEYWORDS receptor-coupled G protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2072)
AUTHORS Lomanev, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
Yang, F., T.L., Caron, M.G., and Lefkowitz, R.J.
TITLE Expansion of the alpha-2-adrenergic receptor family: cloning and
characterization of a human alpha-2-adrenergic receptor subtype,
the gene for which is located on chromosome 2
Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
JOURNAL 90311349
MEDLINE 2164221
COMMENT Original source text: Human placenta DNA, clone alpha-2 C2.
Draft entry and computer-readable sequence for (1) kindly submitted
by J.W.Lomanev, 03-MAY-1990, for release after publication.

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BASE COUNT 316 a 705 c 660 g 391 t
ORIGIN Chromosome 2..

Query Match 67.1%; Score 902; DB 9; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACACACGAGACCCCTACTCGTGACAGGACGAGCGGACATGAGCGGCGCATCAC 60
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Db 413 ATGACACACGAGACCCCTACTCGTGACAGGACGAGCGGACATGAGCGGCGCATCAC 472

QY 61 TTCTCATCTCTTTACATCTTCGACAGGCTTGCTATCTCGGCTGTGTGACACG 120
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Db 473 TTCTCATCTCTTTACATCTTCGACAGGCTTGCTATCTCGGCTGTGTGACACG 532

QY 121 CGCTCGCTGCGCGCCCTCAGAACTGTCTCTGCTGTGCGTGGCGCGCCGACATCTG 180
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Db 533 CGCTCGCTGCGCGCCCTCAGAACTGTCTCTGCTGTGCGTGGCGCGCCGACATCTG 592

QY 181 GTGGCAGAGCTATCATCTCTTTCTGCTGACCAAGAGTGTGGGCTACTGTACTTC 240
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QY 241 CGGCGACGCGTGGCGAGGAGGTACTCTGCGGCTGACGCTGCTCTTGCACCTGTCATC 300
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QY 361 AATCCAGAGGACCCCGCGCGCATCAAGTGCATATCTCACTGTGTGCTCATGCGC 420
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Db 1013 CGGAGAACCGGAGAGTCCGAGGCGGAGGCGGCGGCGGAGGAGTGAATCAGAGAG 1072

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QY 721 GCTTTCGACAGAGAGTCAACGACACTCGAAGTCCACTGAGGAGAGAGAGAGGAGAG 780
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Db 1133 GCTTTCGACAGAGAGTCAACGACACTCGAAGTCCACTGAGGAGAGAGAGAGGAGAG 1192

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QY 841 GGCACAGGCGAGAGAGGGGTGTTGTGGGCGATCTCCAGAGATGAAGCTGAAGAGAG 900
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QY 901 GA 902
|||
Db 1313 GA 1314

RESULT 7
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LOCUS Sequence 41 from Patent WO02061087.
DEFINITION AX548756
ACCESSION AX548756.1 GI:25813686
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Burner, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides

Mon Feb 9 08:28:40 2004

us-09-692-077d-2.01igo.rge

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QY 898 GAGGA 902
Db 616 GAGGA 620

RESULT 10
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DEFINITION alpha 2-adrenergic receptor [rats, Sprague-Dawley, isolets of Langerhans, mRNA partial, 828 nt].
ACCESSION S67316.1 GI:456949
VERSION S67316
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 828)
AUTHORS Wang S.Y. and Pilkey, D.T. of Langerhans of a new rat alpha 2-adrenergic receptor
TITLE Identification in isolets of Langerhans of a new rat alpha 2-adrenergic receptor
JOURNAL Dissect 43 (1), 127-136 (1994)
MEDLINE 9408569
PUBMED 8262309
REMARK Genbank staff at the National Library of Medicine created this entry [NCBI gi456949] from the original journal article.
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Best Local Similarity 99.5%; Pred. No. 4,8e-278; Indels 0; Gaps 0;
Matches 758; Conservative 0; Mismatches 4;
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Db 82 AAGCGACCCCGCGCGCGCATCAAGTGCATCTCTCACTGTGGCTCATGCGCGCTC 141
QY 427 ATCTGCTGCGCGCGCGCTCATCAAGGGCGACGAGGCGCCCGCGCGCGCGCC 201
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QY 607 AACCGAGAGGTCCAGGGCGCCAGGGGGGCGTGGCAGAGTGAATCCAGACGCCGA 666
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QY 727 GCCAGAGAGTCAACGAGCATCAAGTCACTGGGAGAGAGAGAGAGAGAGAGAGAG 501
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RESULT 11
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LOCUS HSA325747
DEFINITION Homo sapiens genomic sequence surrounding Not1 site, clone
VERSION AJ325747
ACCESSION AJ325747.1 GI:15870141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1030)
AUTHORS Kutsenko, A.S., Gishatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podolsky, R.M., Matushkin, Y.G., Ganchandany, A., Muravenko, V.I., Levitsky, V.G., Kolobanov, N.A., Protodopov, A.I., Khashuba, V.I., Kiselev, L.L., Wasserman, W., Wahlstedt, C. and Zabarovsky, E.R.
TITLE Not1 flanking sequences: a tool for gene discovery and verification of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 1030)
AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorigenology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden

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Job time : 5089.47 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:51:07 ; Search time 394.679 Seconds
(without alignments)
9192.405 Million cell updates/sec

Title: US-09-692-077D-2

Perfect score: 1344

Sequence: 1 atgagaccaccagagaccctca.....ggaccacagacggcctcgtga 1344

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 30

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_19jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1344 | 100.0 | 1344 | 23 | AA199906 Human alpha-2BAR c |
| 2 | 1191 | 88.6 | 1344 | 22 | AA004761 Human alpha2B-adre |
| 3 | 1191 | 88.6 | 1344 | 24 | AA044388 Human alpha-2B-adre |
| 4 | 902 | 67.1 | 1353 | 22 | AA004762 Human alpha-2BAR c |
| 5 | 902 | 67.1 | 1353 | 23 | AA199905 Human alpha-2BAR c |
| 6 | 902 | 67.1 | 1353 | 24 | AA044389 Human alpha-2B-adr |
| 7 | 902 | 67.1 | 2072 | 25 | ACA56583 Human signalling p |
| 8 | 902 | 67.1 | 3274 | 25 | ABZ42624 Human alpha 2b-adr |

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| 9 | 522 | 38.8 | 2064 | 12 | AA014151 Human alpha 2 beta |
| 10 | 522 | 38.8 | 2064 | 18 | AA059499 Human alpha-2b adr |
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| 12 | 60 | 4.5 | 60 | 24 | ABN46479 Human spliced tran |
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| 14 | 45 | 3.3 | 1350 | 23 | AA199918 Human alpha-2BAR v |
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| 22 | 34 | 2.5 | 1383 | 23 | AA199931 Human alpha-2CAR e |
| 23 | 34 | 2.5 | 2826 | 25 | ABZ42625 Human alpha 2c-adr |
| 24 | 33 | 2.5 | 6904 | 24 | ABJ32075 Human immune syste |
| 25 | 33 | 2.5 | 6904 | 24 | ABZ35365 Human chemically t |

ALIGNMENTS

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RESULT 1
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AC AA199906;
XX
DT 18-FEB-2002 (first entry)
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DE Human alpha-2BAR third intracellular loop variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1344
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FT FT /note= "sequence is deleted for a 9 nucleotide
FT FT polymorphic site found at nucleotides 901-903
FT FT of the wildtype alpha-2BAR protein (AA199905)"
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PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US12575.
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PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
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PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI, 2001-611728/70.
DR P-PSDB; AAM52118.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Claim 5; Page 144-145; 163pp; English.
XX
XX The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
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sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;

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| Query Match | 100.0% | Score 1344; | DB 23; | Length 1344; |
| Best Local Similarity | 100.0% | Pred. No. 0; | | |
| Matches 1344; | Conservative | | | |

| QY | conservative | mismatches | indels | Gaps |
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121 CGCTCGCTGCGCGCCCCCTCAGAACCTGTTCTGCTGTCGCTGCGCGCGCGCGACATCCTG 180

181 GTGGCCACGCTCATATCCCTTTCTCGGTGGCCACAGAGCTGCTGGGCTACTGGTACTTTC 240

241 CGGCGACGTGTGCGAGGTACCTGGCGTGGACGTCCTTTTGACACCTGTCATC 300
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303 GTGCACTGTGCGCATACGCTGGACCGCTACTGAGCGCGTGAACCGCGGCGCTGAGTAC 360

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| XX | WO200129082-A1. |
| XX | 26-APR-2001. |
| XX | 20-OCT-2000; 2000MO-F100913. |
| XX | 22-OCT-1999; 99US-0422985. |
| XX | (JUVVA-) JUVANTIA PHARMA LTD OY. |
| XX | Snapiir A., Heinoenen P., Alhopuro P., Karvonen M., Koulu M., Pesonen U; |
| XX | Salonen M., Salonen J.T., Tuomainen T., Lakka TA., Nyyssönen K; |
| XX | Salonen R., Kaunonen J., Valkonen V; |
| XX | WPI; 2001-300318/31. |
| XX | P-PSDB; AAE00989. |
| XX | New DNA molecule encoding variant specific adrenoceptor protein with |
| XX | deletion of specific amino acids located in the third intracellular |
| XX | loop of the polypeptide, for treating vascular contraction of coronary |
| XX | arteries - |
| XX | Claim 3; Page 24-26; 37pp; English. |
| XX | The present sequence is a gene encoding human alpha2B-adrenoceptor |
| XX | (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat |
| XX | element (amino acids 298-309) of 12 glutamates, in an acidic stretch of |
| XX | 18 amino acids (amino acids 294-311), located in the third intracellular |
| XX | loop of the receptor polypeptide. The variant is obtained by deletion of |
| XX | three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR |
| XX | gene is located on chromosome 2. Alpha2-AR mediate many of the |
| XX | physiological effects of the catecholamines, norepinephrine and |
| XX | epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating |
| XX | a mammal suffering from vascular contraction of coronary arteries and a |
| XX | disease involving vascular contraction of coronary arteries which is |
| XX | clinically expressed as coronary heart disease (CHD), unstable chronic |
| XX | angina pectoris which is clinically expressed as Prinzmetal's variant |
| XX | form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in |
| XX | gene therapy. |
| XX | Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other; |
| XX | Query Match 88.6%; Score 1191; DB 22; Length 1344; |
| XX | Best Local Similarity 99.8%; Pred. No. 0. |
| XX | Matches 1341; Conservative 0; Mismatches 3; Indels 0; Gaps 0. |
| QY | 1 ATGAGCACACGAGACCCTACTCTCGTGCAGGCGCACAGCGGCGGCATACACC 60 |
| DB | 1 ATGAGCACACGAGACCCTACTCTCGTGCAGGCGCACAGCGGCGGCATACACC 60 |
| QY | TTCCCATCTCTTACCATCTTTGGCAACGCTCGTGCATCTCGGCTGTGTGACACGC 120 |
| DB | TTCCCATCTCTTACCATCTTTGGCAACGCTCGTGCATCTCGGCTGTGTGACACGC 120 |
| QY | CGCTCGTGCAGCGCCCTCAGAACCTGTTCCTGTGTGCTGCGTGGCCGCGCGACATCTGTG 180 |
| DB | CGCTCGTGCAGCGCCCTCAGAACCTGTTCCTGTGTGCTGCGTGGCCGCGCGACATCTGTG 180 |
| QY | GTGGCGACGCTCATCATCTCTTCTCGTGCAGCAAGACTGCTGAGGCTACTGTGATCTTC 240 |
| DB | GTGGCGACGCTCATCATCTCTTCTCGTGCAGCAAGACTGCTGAGGCTACTGTGATCTTC 240 |
| QY | CGGCGCAGTGTGTGAGGTGTGACCTGTGCGCTCGACAGTGTCTTCTTGACCTCTGTCAATC 300 |
| DB | CGGCGCAGTGTGTGAGGTGTGACCTGTGCGCTCGACAGTGTCTTCTTGACCTCTGTCAATC 300 |
| QY | GTGCACCTGTGTGCGCATCAGCTGTGACCGCTTACTGGGCGCTGTGAGCCGCGCTGTGAGTAC 360 |
| DB | GTGCACCTGTGTGCGCATCAGCTGTGACCGCTTACTGGGCGCTGTGAGCCGCGCTGTGAGTAC 360 |
| QY | AACCTCAAGCGCACCCCGCGCGCATCAAGTGCATCATCTTCATCTGTGTGCTCATCGCC 420 |

| | | | |
|----|------|--|------|
| Db | 361 | AACCTCAAGGSCACCCCGCGCCGATCAAGTGATCATCTCTCATCTGTGTGGCTATCGCC | 420 |
| Oy | 421 | GCCGTCATCTCGCTGCCGCCCTTCATCTACAGGGGCAACAGGGCCCCAGCGCGGG | 480 |
| Db | 421 | GCCGTCATCTCGCTGCCGCCCTTCATCTACAGGGGCAACAGGGCCCCAGCGCGGG | 480 |
| Oy | 481 | CGCCCCAGTGCAGAGCTCAACCAAGAGGCGCTGTATACATCTCGGCTCCAGATGGAGCT | 540 |
| Db | 481 | CGCCCCAGTGCAGAGCTCAACCAAGAGGCGCTGTATACATCTCGGCTCCAGATGGAGCT | 540 |
| Oy | 541 | TTCTTTGCTCTTGCTCTCATCATGATCTCTGTCTAACCTGGCATCTACCTGATCGCAAA | 600 |
| Db | 541 | TTCTTTGCTCTTGCTCTCATCATGATCTCTGTCTAACCTGGCATCTACCTGATCGCAAA | 600 |
| Oy | 601 | CGAGCAACCGCAGAGGTCCCAAGGGGCAACAGGGGGGCGCTGGGCAAGGATGCACAG | 660 |
| Db | 601 | CGAGCAACCGCAGAGGTCCCAAGGGGCAACAGGGGGGCGCTGGGCAAGGATGCACAG | 660 |
| Oy | 661 | CCCCGACCCCACTATGTTGGGGCTTTTGGGCTTCAGCCAACTGCCAGCCCTGTGTG | 720 |
| Db | 661 | CCCCGACCCCACTATGTTGGGGCTTTTGGGCTTCAGCCAACTGCCAGCCCTGTGTG | 720 |
| Oy | 721 | GCTTCTGCAAGAGGTCAACGCACTCCAGTCCAGTCCAGTGGGAGGAGAGGGAG | 780 |
| Db | 721 | GCTTCTGCAAGAGGTCAACGCACTCCAGTCCAGTCCAGTGGGAGGAGAGGGAG | 780 |
| Oy | 781 | ACCCCTGAGATACCTGGGACCCCGGGCTTGGCAACCAGTTGGGCTGCTTCCCACTCA | 840 |
| Db | 781 | ACCCCTGAGATACCTGGGACCCCGGGCTTGGCAACCAGTTGGGCTGCTTCCCACTCA | 840 |
| Oy | 841 | GGCCAGGGCCAGAGAGAGGTGTTTGTGGGGCATCTCCAGATGAAAGTGAAGAGAG | 900 |
| Db | 841 | GGCCAGGGCCAGAGAGAGGTGTTTGTGGGGCATCTCCAGATGAAAGTGAAGAGAG | 900 |
| Oy | 901 | GAGAGAGGAGAGGAAAGTGTGAACCCCAAGGCAATGCAAGTGTCCGGGCTCAGCTTGC | 960 |
| Db | 901 | GAGAGAGGAGAGGAGAGTGTGAACCCCAAGGCAATGCAAGTGTCCGGGCTCAGCTTGC | 960 |
| Oy | 961 | AGCCCCCGCTGACAGACGCAACAGGGCTCCGGGTGCTGGCACTTACGTGGCAAGTG | 1020 |
| Db | 961 | AGCCCCCGCTGACAGACGCAACAGGGCTCCGGGTGCTGGCACTTACGTGGCAAGTG | 1020 |
| Oy | 1021 | CTCTGAGGAGGGGCGTGGTGTCTATATAGTGGGCAATGATGGGCTGCAGAGGGCGACCTG | 1080 |
| Db | 1021 | CTCTGAGGAGGGGCGTGGTGTCTATATAGTGGGCAATGATGGGCTGCAGAGGGCGACCTG | 1080 |
| Oy | 1081 | ACCCGGGAGAAAGCGCTTCACTTGTGTCTGGCTGTGTCAATGGCGTTTTTGTGCTCTGC | 1140 |
| Db | 1081 | ACCCGGGAGAAAGCGCTTCACTTGTGTCTGGCTGTGTCAATGGCGTTTTTGTGCTCTGC | 1140 |
| Oy | 1141 | TGTTTCCCTTCTTCTTCAAGCTACAGCCTGGGCGCATCTGGCCGGAAGCACTGCAAGTG | 1200 |
| Db | 1141 | TGTTTCCCTTCTTCTTCAAGCTACAGCCTGGGCGCATCTGGCCGGAAGCACTGCAAGTG | 1200 |
| Oy | 1201 | CCCCATGGGCTCTTCCAGTTCCTTCTTCTGATGGCTACTGCAACACACTCACTGAACCT | 1260 |
| Db | 1201 | CCCCATGGGCTCTTCCAGTTCCTTCTTCTGATGGCTACTGCAACACACTCACTGAACCT | 1260 |
| Oy | 1261 | GTTATCTTACACCATCTTCAACCAAGACTTCCGCGTGTCTTCCGAGAGATCTGTGCCG | 1320 |
| Db | 1261 | GTTATCTTACACCATCTTCAACCAAGACTTCCGCGTGTCTTCCGAGAGATCTGTGCCG | 1320 |
| Oy | 1321 | CCGTGGAACCCAGACGGGCTGGTGA | 1344 |
| Db | 1321 | CCGTGGAACCCAGACGGGCTGGTGA | 1344 |

[illegible][illegible]

RESULT 4

AD04762
ID AAD04762 standard; DNA; 1353 BP.
XX
AC AAD04762;
XX
DT 04-JUL-2001 (first entry)
DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
KW Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
norepinephrine; epinephrine; therapy; vascular contraction;
coronary artery; coronary heart disease; CHD; chronic angina pectoris;
acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
protein"
XX
XX MO200129082-A1.
XX
XX 26-APR-2001.
XX
XX 20-OCT-2000; 2000MO-F100913.
XX
XX 22-OCT-1999; 99US-0422985.
XX
XX (JUVVA-) JUVANTIA PHARMA LTD OY.
XX
XX Snaþir A., Heimonen P., Alhopuro P., Karvonen M., Koulou M., Pesonen U;
PI Scheinin M., Salonen JT., Tuomainen T., Lakka TA., Nyssönen K;
PI Salonen R., Kahanen J., Valkonen V;
XX
XX WPI; 2001-300318/31.
XX
XX P-PSDB; AAE00990.
XX
XX New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular
PT loop of the polypeptide, for treating vascular contraction of coronary
PT arteries -
XX
XX Disclosure; Page 27-29; 37pp; English.
XX
XX The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
CC acids (amino acids 294-311), located in the third intracellular loop of
CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
CC Alpha2-AR mediate many of the physiological effects of the
CC catecholamines, norepinephrine and epinephrine. An antagonist of
CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
CC vascular contraction of coronary arteries and a disease involving
CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
CC clinically expressed as Prinzmetal's variant form or acute myocardial
CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
XX
XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
SO

Query Match 67.1%; Score 902; DB 22; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACACGAGGACCCCTACTCCGCGACGCGACGCGGCTTACGCGGCGGATCACC 60
DB 1 ATGGACACGAGGACCCCTACTCCGCGACGCGACGCGGCTTACGCGGCGGATCACC 60
QY 61 TTCCTCATCTCTTTTACCATCTTGGCAACGCTGTGTCATCTGCTGTGTGACACAG 120
|||||

DB 61 TTCCTCATCTCTTTTACCATCTTGGCAACGCTGTGTCATCTGCTGTGTGACACAG 120
QY 121 CGCTCGTGCGGCGCCCTCAGAACCTGTTCTGCGTGTGCGCGCGCGCATCTCG 180
DB 121 CGCTCGTGCGGCGCCCTCAGAACCTGTTCTGCGTGTGCGCGCGCGCATCTCG 180
QY 181 GTGGCCACGCTCATCATCCCTTTCTGCGGCCCAAGAGCTGTGGGCTACTGTAATTG 240
DB 181 GTGGCCACGCTCATCATCCCTTTCTGCGGCCCAAGAGCTGTGGGCTACTGTAATTG 240
QY 241 CGGCGACGCTGTGCGGAGGTGTAACCTGCGGCTGACGCTGCTTCTGCACTCTGTCATC 300
DB 241 CGGCGACGCTGTGCGGAGGTGTAACCTGCGGCTGACGCTGCTTCTGCACTCTGTCATC 300
QY 301 GTGCACCTGTGCGGCACTGACCGCTGACCGGCTAATGCGGCGGCGGCGGAGTAC 360
DB 301 GTGCACCTGTGCGGCACTGACCGCTGACCGGCTAATGCGGCGGCGGCGGAGTAC 360
QY 361 AACTCGAAGCGACCCCGCGCGCATCAAGTGCATCTCTGCTGTGCTCATCTGCGC 420
DB 361 AACTCGAAGCGACCCCGCGCGCATCAAGTGCATCTCTGCTGTGCTCATCTGCGC 420
QY 421 GCGGTATCTGCTGCTGCGCGCGCTCATCTCAAGGCGGACCGGCGCGCGCGG 480
DB 421 GCGGTATCTGCTGCTGCGCGCGCTCATCTCAAGGCGGACCGGCGCGCGCGG 480
QY 481 CGGCGGACGAGGCTCAACGAGGAGGCTGTGTAATCTGCGCTTCCAGATCGATCT 540
DB 481 CGGCGGACGAGGCTCAACGAGGAGGCTGTGTAATCTGCGCTTCCAGATCGATCT 540
QY 541 TTCTTGTCTCTTCTGCTCATCATGATCTTGTCTTACCTGCGCATCTACCTGATCGCAAA 600
DB 541 TTCTTGTCTCTTCTGCTCATCATGATCTTGTCTTACCTGCGCATCTACCTGATCGCAAA 600
QY 601 CGCAGCAACCGCAGAGGCTCCAGAGGCGCAAGGCGGCGCTTGGCGAGGTGCAAGCAG 660
DB 601 CGCAGCAACCGCAGAGGCTCCAGAGGCGCAAGGCGGCGCTTGGCGAGGTGCAAGCAG 660
QY 661 CCCGACCCGACCATGATGAGGCTTGTGCTTCAAGCCAACTGCGACGCTTGGCTGTG 720
DB 661 CCCGACCCGACCATGATGAGGCTTGTGCTTCAAGCCAACTGCGACGCTTGGCTGTG 720
QY 721 GCTTTCGACAGAGGCTCAACGCACTCGAAGTCCATGCGGAGAGAGAGGAGGAG 780
DB 721 GCTTTCGACAGAGGCTCAACGCACTCGAAGTCCATGCGGAGAGAGAGGAGGAG 780
QY 781 ACCCTGAAAGATATCTGGGACCGGCGCTTGCACCAAGTTGGGCTGCCCTTCCCACTGA 840
DB 781 ACCCTGAAAGATATCTGGGACCGGCGCTTGCACCAAGTTGGGCTGCCCTTCCCACTGA 840
QY 841 GGCAGAGGCGCAAGAGAGGCTTGTGCGGCTTCCAGAGATGAGTGAAGAGAG 900
DB 841 GGCAGAGGCGCAAGAGAGGCTTGTGCGGCTTCCAGAGATGAGTGAAGAGAG 900
QY 901 GA 902
DB 901 GA 902

RESULT 5
AAI99905
ID AAI99905 standard; DNA; 1353 BP.
XX
AC AAI99905;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
polymorphic site; allelic variant; cardiovascular disease;
central nervous system disease; adenylyl cyclase; MAP kinase activity;
phosphorylation; inositol phosphate; alpha-2BAR;


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XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT CDS 1..1353
XX FT /tag a
XX FT /product= "Human alpha-2B-adrenoceptor protein"
XX PN WO200266617-A1.
XX PD 29-AUG-2002.
XX PF 13-FEB-2002; 2002WO-FI00113.
XX PR 20-FEB-2001; 2001FI-0000323.
XX PA (JURI-) JURILAB LTD OY.
XX PI Salonen J;
XX DR WPI; 2002-667063/71.
XX DR P-PSDB; AAE26634.
XX PT Detecting a risk of hypertension and targeting treatment in a subject
XX PT by determining the pattern of alleles encoding a variant
XX PT alpha-2-adrenoceptor
XX PS Disclosure; Page 27-29; 35pp; English.
XX CC The invention relates to a method for detecting a risk of hypertension
XX CC by determining the pattern of alleles encoding a variant alpha-2B-
XX CC adrenoceptor (AR) protein. The methods and compositions of the invention
XX CC are useful for detecting risks and targeting treatment for hypertension.
XX CC The kit is also useful for selecting for clinical drug trials testing
XX CC the antihypertensive effect of compounds. The present sequence is human
XX CC alpha-2B-adrenoceptor gene.
XX SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;

Query Match 67.1%; Score 902; DB 24; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCACAGAGACCCCTACTCCGTCAGGCGACAGCGGCATAGCGGCGCATCACC 60
DB 1 ATGAGCACAGAGACCCCTACTCCGTCAGGCGACAGCGGCATAGCGGCGCATCACC 60
QY 61 TTCCTCATTTCTTTACCATCTTTCGCAACGCTTGTGTCATCTGCTGTGTTGACCAAC 120
DB 61 TTCCTCATTTCTTTACCATCTTTCGCAACGCTTGTGTCATCTGCTGTGTTGACCAAC 120
QY 121 CGCTGCTGCGCGCCCTTCAGAACTGTTCTGTGTCTGTGTCGCGCGCGACATCTCTG 180
DB 121 CGCTGCTGCGCGCCCTTCAGAACTGTTCTGTGTCTGTGTCGCGCGCGACATCTCTG 180
QY 181 GTGGCAGCGTCATATCCCTTTCTGTGCGCAAGAGCTGTGGGCTACTGTAATCTTC 240
DB 181 GTGGCAGCGTCATATCCCTTTCTGTGCGCAAGAGCTGTGGGCTACTGTAATCTTC 240
QY 241 CGGCGCAGTGTGCGAGGTGTACTGCGCTGACGCTCTTCTGTGCACTCGTCCATC 300
DB 241 CGGCGCAGTGTGCGAGGTGTACTGCGCTGACGCTCTTCTGTGCACTCGTCCATC 300
QY 301 GTGCACTGTGTGCGCATCAGCTTGACCGCTACTGCGCGGTGAGCGCGCTGAGTAC 360
DB 301 GTGCACTGTGTGCGCATCAGCTTGACCGCTACTGCGCGGTGAGCGCGCTGAGTAC 360
QY 361 AACTCAGAGCGACCCCGCGCGCATCAAGTGCATCTTCACTGTGTGCGTCAATCGCC 420
DB 361 AACTCAGAGCGACCCCGCGCGCATCAAGTGCATCTTCACTGTGTGCGTCAATCGCC 420
QY 421 GCCGTCATCTCGCTCGCGCCCTTCATCTCAAGGCGACCAAGGCGCGCGCGCGG 480

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DB 421 GCCGTCATCTCGCTCGCGCCCTTCATCTCAAGGCGACCAAGGCGCGCGCGCGG 480
QY 481 CGCCCCAGTGAAGCTCAACAGAGAGCGCTGTATATCTGTGCGCTCAAGCATCGATCT 540
DB 481 CGCCCCAGTGAAGCTCAACAGAGAGCGCTGTATATCTGTGCGCTCAAGCATCGATCT 540
QY 541 TTCTTGTCTCTTGTGCTCATCATGATCTTGTCTTACCTGCGCATCTACCTGATCGCAAA 600
DB 541 TTCTTGTCTCTTGTGCTCATCATGATCTTGTCTTACCTGCGCATCTACCTGATCGCAAA 600
QY 601 CGAGCAACCGCAAGGTCCAGGCGCAAGGCGGCGCTGTGCGAGGTGATCAAGCAG 660
DB 601 CGAGCAACCGCAAGGTCCAGGCGCAAGGCGGCGCTGTGCGAGGTGATCAAGCAG 660
QY 661 CCCGACCCGACCAATGTGGGCTTTGTGCTCAGGCCAATCTGCGAGCTGTGCTGTG 720
DB 661 CCCGACCCGACCAATGTGGGCTTTGTGCTCAGGCCAATCTGCGAGCTGTGCTGTG 720
QY 721 GCTTGTCCAGAGAGTCAACGAGCACTTCAAGTCCACTGTGGGAGAGAGAGGAGGAG 780
DB 721 GCTTGTCCAGAGAGTCAACGAGCACTTCAAGTCCACTGTGGGAGAGAGAGGAGGAG 780
QY 781 ACCCTGAAGATATCTGAGACCCGCGCTTGCACCCAGTTGGGCTGCTTCCAACTCA 840
DB 781 ACCCTGAAGATATCTGAGACCCGCGCTTGCACCCAGTTGGGCTGCTTCCAACTCA 840
QY 841 GGCAGGCGCAGAGAGAGGTGTTTGTGGGCACTTCCAGAGATCAACTGAAGAGAG 900
DB 841 GGCAGGCGCAGAGAGAGGTGTTTGTGGGCACTTCCAGAGATCAACTGAAGAGAG 900
QY 901 GA 902
DB 901 GA 902

RESULT 7
ID ACAS6583
ACAS6583 standard; cDNA; 2072 BP.
ACAS6583;
06-JUN-2003 (first entry)
XX DE Human signalling pathway polynucleotide probe SEQ ID NO 1181.
XX KW Human; probe; ss; array element; Parkinson's disease;
XX KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
XX KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX OS Homo sapiens.
XX PN US6500938-B1.
XX PD 31-DEC-2002.
XX PF 30-JAN-1998; 98US-0016434.
XX PR 30-JAN-1998; 98US-0016434.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Au-Young J; Seilhamer J;
XX DR WPI; 2003-352189/33.
XX PT Combination of polynucleotide probes, useful as array elements in a
XX PT microarray for monitoring the expression of a number of target
XX PT polynucleotides -
XX PS Claim 1; SEQ ID NO 1181; 65pp; English.
XX CC The invention relates to a combination which, comprises a number of
XX CC polynucleotide probes comprising a sequence selected from one of the 1490

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sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neurodegenerative diseases, Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=0650093801.

Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other;

| | | | | |
|---------------------------|--------|--------------|--------|-------------------|
| Query Match | 67.1% | Score 902; | DB 25; | Length 2072; |
| Best Local Similarity | 100.0% | Pred. No. 0; | | |
| Matches 902; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0; |

| | | | |
|----|------|--|------|
| OY | 1 | ATGACACACCAAGACCCCTTACTTCGGTAGAGGCAACAGGGGCAATAGACGGGGCCATCAAC | 60 |
| Db | 413 | ATGGACCAACAAGACCCCTACTACTCGTAGAGGCAACAGCGGCAATAGCGGGCCATCAACC | 472 |
| OY | 61 | TTTCATCATTCCTGTTTACATCTTGGCAACGCTCTGATCATCTTGAGTGTGTTCACAGC | 120 |
| Db | 473 | TTTCATCATTCCTTTTACCATCTTCGGCAACGCTCTGATCATCTTGAGTGTGTTCACAGC | 532 |
| OY | 121 | CGCTGGCTGCGGCGCCCTCAGAACCTGTTCTTGATGTGCTGAGCGCGCCGACATCCTG | 180 |
| Db | 533 | CGCTGGCTGCGGCGCCCTCAGAACCTGTTCTTGATGTGCTGAGCGCGCCGACATCCTG | 592 |
| OY | 181 | GTGGCCACGCTCATATATCCCTTTCTGCGTAGGCAACAGACTCTGGGCTCATGTGATCTT | 240 |
| Db | 593 | GTGGCCACGCTCATATATCCCTTTCTGCGTAGGCAACAGACTCTGGGCTCATGTGATCTT | 652 |
| OY | 241 | CGGCGCACGTGGTGCGAGGTGTACCTGAGCGCTCGACGTCTCTTCTGCACCTCGTTCATC | 300 |
| Db | 653 | CGGCGCACGTGGTGCGAGGTGTACCTGAGCGCTCGACGTCTCTTCTGCACCTCGTTCATC | 712 |
| OY | 301 | GTGCACTCTGTGCGCATCAAGCCTTGAACGCGCTACTGGGCGGTGAGCCGCGCTTGAGATAC | 360 |
| Db | 713 | GTGCACTCTGTGCGCATCAAGCCTTGAACGCGCTACTGGGCGGTGAGCCGCGCTTGAGATAC | 772 |
| OY | 361 | AACTCCAAAGCGCAACCCCGCGCGGCATCAAGTAGATATCCCTCATCTGTGTGGCTCAATCGCG | 420 |
| Db | 773 | AACTCCAAAGCGCAACCCCGCGCGGCATCAAGTAGATATCCCTCATCTGTGTGGCTCAATCGCG | 832 |
| OY | 421 | GCGGTATCTCGCTGCGCGCCCTCATCTCAAGAGGCGCAACAGGAGCCCGACGCGCGGAG | 480 |
| Db | 833 | GCGGTATCTCGCTGCGCGCCCTCATCTCAAGAGGCGCAACAGGAGCCCGACGCGCGGAG | 892 |
| OY | 481 | CGCCCCAGTGCAGGCTCAACAGAGAGGCTGTGATCATCTGGCTTCAGCATCGGATCT | 540 |
| Db | 893 | CGCCCCAGTGCAGGCTCAACAGAGAGGCTGTGATCATCTGGCTTCAGCATCGGATCT | 952 |
| OY | 541 | TTCTTTGCTCCTTGCCCTCATCAAGATCCTGTCTACTGCGATCTAACCGATTCGCGCAA | 600 |
| Db | 953 | TTCTTTGCTCCTTGCCCTCATCAAGATCCTGTCTACTGCGATCTAACCGATTCGCGCAA | 1012 |
| OY | 601 | CGCAGCAACCGCAGAGGTCCCAAGGCGCAAGAGGAGGAGCTTGAGCAGGTGATCTCAAGAG | 660 |
| Db | 1013 | CGCAGCAACCGCAGAGGTCCCAAGGCGCAAGAGGAGGAGCTTGAGCAGGTGATCTCAAGAG | 1072 |
| OY | 661 | CCCGAACCCGACCATGATGGAGGCTTTGACCTCAACCAACTGCGACGCTTGACTGTG | 720 |

| | | | |
|----|------|--|------|
| Dd | 1073 | CCCCGACCCGACCATGGTGGGGGCTTTGGCTCAGCCAAATCTGCACGCCCTGGCTCTGTG | 1132 |
| Qy | 721 | GCTTCTCCGAGAGGGTCTCAACGACACTCGAAGTCTCACTGGGAGGAAGAGAGAGGGGAG | 780 |
| Dd | 1133 | GCTTCTCCGAGAGGGTCTCAACGACACTCGAAGTCTCACTGGGAGGAAGAGAGAGGGGAG | 1192 |
| Qy | 781 | ACCCCTGAAGAATACTGGGGAACCCGGGCGCTTGCGACCTCGAGTTGGGCGTGCCTTCCCAACTCA | 840 |
| Dd | 1193 | ACCCCTGAAGAATACTGGGGAACCCGGGCGCTTGCGACCTCGAGTTGGGCGTGCCTTCCCAACTCA | 1253 |
| Qy | 841 | GGCCAGGGCCGAGAGAGAGGAGTGTTTGTGGGCACTCTCAGAGATGAAGCTGAAGAGGAG | 900 |
| Dd | 1253 | GGCCAGGGCCGAGAGAGAGGAGTGTTTGTGGGCACTCTCAGAGATGAAGCTGAAGAGGAG | 1312 |
| Qy | 901 | GA 902 | |
| Dd | 1313 | GA 1314 | |

RESULT 8
AD7A2C34

ABZ42624
ID ABZ42624 standard; DNA; 3274 BP

AC ABZ42624

DT 04-MAR-2003 (first entry)

Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41

G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 G-protein-coupled receptor modulator; antibody; immune-related disease;
 growth-related disease; cell regeneration-related disease; AIDS; cancer;
 immunologic-related cell proliferative disease; autoimmune disease;
 Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy
 osteoporosis; cardiovascularity; inflammation; Crohn's disease; diabetes;
 graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 ulcer; ds.

Homo sapiens

PN WO200261087-A2

08-AUG-2002.

19-DEC-2001; 2001WO-US50107.

PR 19-DEC-2000; 2000US-257144P

(LIFE-) LIFESPAN BIOSCIENCES INC

PI Burner GC, Roush CL, Brown JP,

DR WPI; 2003-046718/04

XX : 100

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -

PS Disclosure; Fig 1; 523pp; English

The present invention describes antigenic peptides (I) comprising:
 (a) any one of 1601 sequences (see ABP92019 to ABP93619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G-protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity and avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific

antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ43523 to ABZ4869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.

80 Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 other;

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|----------------------|--------|-----------|-------|-------------|
| Query Match | 67.14 | Score 902 | DB 25 | Length 3274 |
| Post-Transcriptional | 100.00 | Score 902 | DB 25 | Length 3274 |

Matches 902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 1 | ATGACACACAGAGACCCCTACTCCGTGACAGGACACAGCGGCATTAACCGGCGGCATACAC | 60 |
| Db | 1 | ATGACACACAGAGACCCCTACTCCGTGACAGGACACAGCGGCATTAACCGGCGGCATACAC | 60 |
| Qy | 61 | TTCTCATCTCTTTACCATCTTTGGCAACGCTCTGTGATCTGTGCTGTGTAGCCAGC | 120 |
| Db | 61 | TTCTCATCTCTTTACCATCTTTGGCAACGCTCTGTGATCTGTGCTGTGTAGCCAGC | 120 |
| Qy | 121 | CGCTGCTGCGCGCCCTCAGAAACCTGTCTCTGAGTCTCGCTGGCGCGCGCGGACATCTCTG | 180 |
| Db | 121 | CGCTGCTGCGCGCCCTCAGAAACCTGTCTCTGAGTCTCGCTGGCGCGCGCGGACATCTCTG | 180 |
| Qy | 181 | GTGGCCAGCTCATCATCTCTTTCTGTGCTGGCCAAAGACCTGCTGGAGCTTACTGTCTTC | 240 |
| Db | 181 | GTGGCCAGCTCATCATCTCTTTCTGTGCTGGCCAAAGACCTGCTGGAGCTTACTGTCTTC | 240 |
| Qy | 241 | CGGCGCAGTGGTGGAGAGGTATACCTGGGGGCTCGAGCTGTCTTTCTTGACCTCGTCACTC | 300 |
| Db | 241 | CGGCGCAGTGGTGGAGAGGTATACCTGGGGGCTCGAGCTGTCTTTCTTGACCTCGTCACTC | 300 |
| Qy | 301 | GTGCACCTGTGGGCATCAGCTGTGACCCGCTACTCTGGGCGCGCGGCTGTGAGTAC | 360 |
| Db | 301 | GTGCACCTGTGGGCATCAGCTGTGACCCGCTACTCTGGGCGCGCGGCTGTGAGTAC | 360 |
| Qy | 361 | AACTCCAAAGCGCACCCCGCGCGGCATCAAGTGATCATCTCTCATCTGTGTGCTCATCGCC | 420 |
| Db | 361 | AACTCCAAAGCGCACCCCGCGCGGCATCAAGTGATCATCTCTCATCTGTGTGCTCATCGCC | 420 |
| Qy | 421 | GGCGTCATCTGCTGCTGGCGCGCCCTCACTCAAGAGGGGAGACAGAGGCCCCAGCGCGCGG | 480 |
| Db | 421 | GGCGTCATCTGCTGCTGGCGCGCCCTCACTCAAGAGGGGAGACAGAGGCCCCAGCGCGCGG | 480 |
| Qy | 481 | CGCCCCCAGTGCAGCTCAACCAAGAGAGGCTGGTACATCTGTGCTCTCGACATCGGATCT | 540 |
| Db | 481 | CGCCCCCAGTGCAGCTCAACCAAGAGAGGCTGGTACATCTGTGCTCTCGACATCGGATCT | 540 |
| Qy | 541 | TTCTTTGTCTCTTGCTCTCATATGATCTTTGTCTACTGTGGCATCTTACTGTATGCGCAA | 600 |
| Db | 541 | TTCTTTGTCTCTTGCTCTCATATGATCTTTGTCTACTGTGGCATCTTACTGTATGCGCAA | 600 |
| Qy | 601 | CGACAGCAACCGCAGAGGTCCACAGGCGCAAGGGGGGGCTGTGGCAGGATGATCTCAAGAC | 660 |
| Db | 601 | CGACAGCAACCGCAGAGGTCCACAGGCGCAAGGGGGGGCTGTGGCAGGATGATCTCAAGAC | 660 |
| Qy | 661 | CCCCGACCCGACCATGTGTGTGGGCTTTGGCTCTACGCCAAACTGCACGCTGTGCTCTGTG | 720 |
| Db | 661 | CCCCGACCCGACCATGTGTGTGGGCTTTGGCTCTACGCCAAACTGCACGCTGTGCTCTGTG | 720 |
| Qy | 721 | GCTTGTGCGAGAGGTCAAAGGACCTGAAAGTCACTGTGGGAGAAAGAGAGAGGAGGAG | 780 |

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| Db | 721 | GCTTTGCGAGAGGATCAACCGACACTTGAAGTCCATTGGGGAGAAAGAGAGGGGAG | 780 |
| Qy | 781 | ACCCCTGAAGATACTGGGACCCGGGCTTGGCACCCAGTTGGGCTCCCTTCCCACTCA | 840 |
| Db | 781 | ACCCCTGAAGATCTGGGACCCGGGCTTGGCACCCAGTTGGGCTCCCTTCCCACTCA | 840 |
| Qy | 841 | GGCCAGGACCAGAGGAGGAGGTTGTGTGGGGCATCTCCAGAGATGAGCTGAAGAGAG | 900 |
| Db | 841 | GGCCAGGACCAGAGGAGGAGGTTGTGTGGGGCATCTCCAGAGATGAGCTGAAGAGAG | 900 |
| Qy | 901 | GA 902 | |
| Db | 901 | GA 902 | |

RESULT 9
AAQ14151
ID AAQ14151 standard; DNA; 2064 BP.

AC AAQ14151;

DT 06-JAN-1992 (first entry)

DE Human alpha 2 beta adrenergic receptor gene.

KW Neurotransmission; adrenaline; epinephrine; NGC-1alpha2beta; ss

Homo sapiens

| FH | Key | Location/Qualifiers |
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FT / *tag= a

PN US5053337-A.

PD 01-OCT-1991.

PF 30-OCT-1989; 89US-0428856.

PR 30-OCT-1989; 89US-042889

PA (NEUR-) NEUROGENETIC CORP.

PI weinshank RL, Hartig PR;

WPI; 1991-310087/42.

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PT nucleic acids encoding all

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| Model | Best Local Similarity | 100.0 |
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| Model 2 | 100.0 | 100.0 |
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| Db | 839 | CCTCATCTACAAGGACACAGAGGCCCCCAGCCCGCGGGGCCCCCAAGTGCACAA | 898 |
| QY | 501 | CCAGGAGGCGCTGGTACATCCCTGAGCTCCAGCATCGATCTTTCTTCTCTGCTCAT | 560 |
| Db | 899 | CCAGAGAGCCCTGGTACATCTTGAGCTCCAGATCGATCTTTCTTCTCTGCTCAT | 958 |
| QY | 561 | CATGATCCTTGTCTACCTGCGCATCTACCTGATGCGCAACGACGAAACCGCAGAGGTCC | 620 |
| Db | 959 | CATGATCTTGTCTACCTGCGCATCTACCTGATGCGCAACGACGAAACCGCAGAGGTCC | 1018 |
| QY | 621 | CAGGCGCCAAAGGGGGGCGCTGAGGCTGAGTCTTCAAGAGGCCCGAACCCGACATGCTGG | 680 |
| Db | 1019 | CAGGCGCCAAAGGGGGGCGCTGAGGCTGAGTCTTCAAGAGGCCCGAACCCGACATGCTGG | 1078 |
| QY | 681 | GCGCTTGGCTCAGCCAAATCTGCCAGCCCTGGCTCTGTGGCTTCTGCCAAGAGGTCAA | 740 |
| Db | 1079 | GCGCTTGGCTCAGCCAAATCTGCCAGCCCTGGCTCTGTGGCTTCTGCCAAGAGGTCAA | 1138 |
| QY | 741 | CGGACACTCGAAGTCACTGCGGGGAGAGAGGAGGGGGAGACCCCTGAAATACTGGGAC | 800 |
| Db | 1139 | CGGACACTCGAAGTCACTGCGGGGAGAGAGGAGGGGGAGACCCCTGAAATACTGGGAC | 1198 |
| QY | 801 | CGGGGCTTGGCCACCACTTGGGCTGCCCTTCCCACTTAGGCGCAGGCGCAGAGAGAGG | 860 |
| Db | 1199 | CGGGGCTTGGCCACCACTTGGGCTGCCCTTCCCACTTAGGCGCAGGCGCAGAGAGAGG | 1258 |
| QY | 861 | TGTTTGTGGGGCATCTCCAGAGGATGAAGCTGAAGAGAGA | 902 |
| Db | 1259 | TGTTTGTGGGGCATCTCCAGAGGATGAAGCTGAAGAGAGA | 1300 |

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| XX | PS | Disclosure, Fig 2A-E, 16pp; English. |
| XX | XX | |
| XX | PT | cells expressing recombinant receptor |
| XX | FT | Assay for alpha-2b adrenergic receptor ligands - using membranes of |
| XX | DR | P-PSDB; AAW1804. |
| XX | DR | WPI; 1997-107576/10. |
| XX | PI | Hartig PR, Weinshank RL; |
| XX | PA | (SYNA-) SYNAPTIC PHARM CORP. |
| XX | XX | |
| XX | PR | 22-OCT-1992; 92US-0965040. |
| XX | PR | 30-OCT-1989; 89US-0428856. |
| XX | PR | 30-MAY-1991; 91US-0707604. |
| XX | PF | 22-OCT-1992; 92US-0965040. |
| XX | PD | 21-JAN-1997. |
| XX | PN | US5595880-A. |
| XX | OS | Homo sapiens. |
| XX | Key | Location/Qualifiers |
| XX | CDS | 288..1751 /*tag= a |
| XX | FT | |
| XX | XX | |
| XX | XX | epinephrine; signal transduction; neurotransmitter; ligand; ss. |
| XX | XX | Alpha-2b adrenergic receptor; adrenoreceptor; adenalinine; |
| XX | DE | Human alpha-2b adrenergic receptor genomic DNA clone. |
| XX | DT | 06-MAY-1997 (first entry) |
| XX | AC | AAT59499; |
| XX | AC | 25-MAR-2003 (updated) |
| XX | ID | AAT59499 standard; DNA; 2064 BP. |
| XX | RESULT 10 | |
| XX | AAT59499 | |

CC A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic
CC receptor (AA011804), a member of the rhodopsin-like signal transducer
CC family. It was isolated from a human spleen genomic library in the
CC lambda vector Charon 28 by screening with a 1.6 kb fragment of the
CC human 5-hydroxytryptamine receptor gene. Plasmid pNC02-alpha-2B
CC comprising DNA encoding the alpha-2B adrenoceptor is deposited as
CC ATCC 68144. Vectors have been adapted to allow produ. of alpha-2B
CC adrenoceptor in bacterial, yeast or mammalian cells; transfected
CC Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL
CC 10275. Membranes of such cells can be used in novel methods to
CC identify drugs which specifically interact with, and bind to, the
CC alpha-2B adrenergic receptor.
CC (Updated on 25-MAR-2003 to correct PF field.)
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CC Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
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| Query Match | 38.8% | Score 522 | DB 18 | Length 2064 |
| Best Local Similarity | 100.0% | Pred. No. 6.3e-230 | | |
| Matches 522 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

| | | | |
|----|------|---|------|
| QY | 361 | CCGACATCAAGGACATCACTCTCAGCTGAGCTCAATATCTCTC | |
| Db | 779 | CCGACATCAAGGACATCACTCTCAGCTGAGCTCAATATCTCTC | 838 |
| QY | 441 | CCTCATCTACAAAGGCGACACGAGGCGCCGAGCGCGCGGCCGCCCAATGTCACAGCTCAA | 500 |
| Db | 839 | CCCTCATCTACAAAGGCGACACGAGGCGCCGAGCGCGCGGCCGCCCAATGTCACAGCTCAA | 898 |
| QY | 501 | CCAGAGAGGCGCTGGTACATCTCGGCTCCGACATCGGATCTTTCTTTCTCTCCTTGCCCTCAT | 560 |
| Db | 899 | CCAGAGAGGCGCTGGTACATCTCGGCTCCGACAGATCGGATCTTTCTTTGCTCTTGGCTCAT | 958 |
| QY | 561 | CATGATCTTTGTTACTCTGCGCATCTACCTGATCGCCAAACGACGAAACCGACAGAGTCC | 620 |
| Db | 959 | CATGATCTTTGTTACTCTGCGCATCTACCTGATCGCCAAACGACGAAACCGACAGAGTCC | 1018 |
| QY | 621 | CAGGCGCAAGGGGGGGGCTGGCGAGGGTGAATCCAAAGACGCCGACCCGACCAATGAGTGG | 680 |
| Db | 1019 | CAGGCGCAAGGGGGGGGCTGGCGAGGGTGAATCCAAAGAGGCCCGACCCGACCAATGAGTGG | 1078 |
| QY | 681 | GGCCTTTGGCTCAGACCCAACTGCGACGCCCTTGACCTCTGTGGCTTCTGCAAGAGTCAA | 740 |
| Db | 1079 | GGCCTTTGGCTCAGACCCAACTGCGACGCCCTTGACCTCTGTGGCTTCTGCAAGAGTCAA | 1138 |
| QY | 741 | CGGACACTCGAATGTCACCTGGGAGAAAGAGAGAGGGGGAGACCCCTTGAAGATACCTGGGAC | 800 |
| Db | 1139 | CGGACACTCGAATGTCACCTGGGAGAAAGAGAGAGGGGGAGACCCCTTGAAGATACCTGGGAC | 1198 |
| QY | 801 | CCGAGGCTTTGCCACCCAGTGGGGCTGSCCTTCCCAACTCAGGCGCAGGGCCAGAGAGAGGG | 860 |
| Db | 1199 | CCGAGGCTTTGCCACCCAGTGGGGCTGSCCTTCCCAACTCAGGCGCAGGGCCAGAGAGAGGG | 1258 |
| QY | 861 | TGTTTGTGGGGCATCTCCAGAGAGTGAAGCTGAAGAGAGAGA | 902 |
| Db | 1259 | TGTTTGTGGGGCATCTCCAGAGAGTGAAGCTGAAGAGAGAGA | 1300 |

| | RESULT 11 |
|----------|---|
| ABN32100 | |
| ID | ABN32100 standard; DNA; 65 BP. |
| XX | |
| AC | ABN32100; |
| XX | |
| DT | 15-JUL-2002 (first entry) |
| XX | |
| DE | Rat spliced transcript detection oligonucleotide SEQ ID NO:4848 |
| XX | |
| KM | Human; mouse; rat; splice transcript; detection; RNA transcript |
| KW | splice variant; transcriptome; oligonucleotide library; ss. |
| XX | |
| OS | Rattus norvegicus. |
| XX | |
| PN | WO200210449-A2. |


```
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-IB01903.
PF
XX 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
DR WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX Example 1; SEQ ID 4848; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 65 BP; 13 A; 22 C; 21 G; 9 T; 0 other;
SQ
XX
XX Query Match 4.8%; Score 65; DB 24; Length 65;
XX Best Local Similarity 100.0%; Pred. No. 1e-19;
XX Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 642 GCAGGCTGACTCCAGAGCCCGACCATGTGGGCTTTGGCTTCAGCCAAACT 701
DB 1 GCAGGGGTGACTCCAGAGCCCGACCATGTGGGCTTTGGCTTCAGCCAAACT 60
QY 702 GCCAG 706
DB 61 GCCAG 65
XX
XX RESULT 12
XX ABN46479
XX ID ABN46479 standard; DNA; 60 BP.
XX AC
XX ABN46479;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:19227.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
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XX OS Homo sapiens.
XX
XX PN NO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 20-JUL-2001; 2001WO-IB01903.
XX
XX PR 28-JUL-2000; 2000US-221607P.
XX PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
DR WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX Example 1; SEQ ID 19227; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 60 BP; 13 A; 20 C; 16 G; 11 T; 0 other;
SQ
XX
XX Query Match 4.5%; Score 60; DB 24; Length 60;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-17;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 698 AACTGCCAGCGCTGCTGTGTGGCTTTCGACAGAGGTCAACGACACTCGAAGTCCA 757
DB 1 AACTGCCAGCGCTGCTGTGTGGCTTTCGACAGAGGTCAACGACACTCGAAGTCCA 60
XX
XX RESULT 13
XX AA19917
XX ID AA19917 standard; DNA; 1350 BP.
XX AC
XX AA19917;
XX
XX 18-FEB-2002 (first entry)
XX
XX Human alpha-2AAR encoding DNA.
XX
XX Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
XX polymorphic site; allelic variant; cardiovascular disease;
XX
```

KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2AR;
 KW GenBank Accession AF281308; chromosome 10; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /tag= a
 FT /product= "alpha-2AR"
 XX
 PN WO200179561-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US12575.
 XX
 PR 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 XX
 DR WPI: 2001-611728/70.
 DR P-PSDB; AAM52122.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Example 7, Page 151; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (999GCG999CG) or (B) (999GCG999G) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AR gene
 CC (GenBank Accession AF281308).
 CC
 SQ Sequence 1350 BP; 199 A; 490 C; 441 G; 220 T; 0 other;
 QY Query Match 3.3%; Score 45; DB 23; Length 1350;
 DB Best Local Similarity 100.0%; Pred. NO. 1.5e-10; Indels 0; Gaps 0;
 Matches 45; Conservative 0; Mismatches 0;
 292 TCGTCATCGTGCACCTGTGCGCATCAGCTGACCGCTACTGCG 336
 355 TCGTCATCGTGCACCTGTGCGCATCAGCTGACCGCTACTGCG 399

ID AA199918 standard; DNA; 1350 BP.
 XX
 AC AA199918;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Human alpha-2AR variant encoding DNA.
 XX
 KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
 KW polymorphic site; allelic variant; cardiovascular disease;
 KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
 KW phosphorylation; inositol phosphate; alpha-2AR; chromosome 10; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /tag= a
 FT /product= "alpha-2AR"
 FT replace(753,C)
 FT allele /tag= b
 XX
 PN WO200179561-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-US12575.
 XX
 PR 17-APR-2000; 2000US-0551744.
 PR 10-AUG-2000; 2000US-0636259.
 PR 19-OCT-2000; 2000US-0692077.
 XX
 PA (LIGG/) LIGGETT S B.
 PA (SMAL/) SMALL K M.
 XX
 PI Liggett SB, Small KM;
 XX
 DR WPI: 2001-611728/70.
 DR P-PSDB; AAM52123.
 XX
 PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
 PT determining whether an individual is at increased risk of developing a
 PT disease associated with the corresponding receptor comprises detecting
 PT a polymorphic site -
 XX
 PS Disclosure; Page 152; 163pp; English.
 XX
 CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
 CC receptor gene (I)-(III) by detecting a polymorphic site, comprising:
 CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
 CC alpha2A or alpha2C or fragment or complement of; and
 CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
 CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
 CC or a site comprising (A) (999GCG999CG) or (B) (999GCG999G) at
 CC positions 961-972 of (III). The method may be used for genotyping an
 CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
 CC whether an individual is at increased risk of developing a disease
 CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
 CC polymorphic site which correlate to disease selected from cardiovascular
 CC disease, central nervous system disease and combinations of these. In
 CC addition, the technique may be used to predict an individual's response
 CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. epinephrine,
 CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
 CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
 CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
 CC these) by detecting the polymorphic site and correlating the site to a
 CC predetermined response (where the response is correlated to adenylyl
 CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
 CC levels). The present sequence is that of the human alpha-2AR variant
 CC gene.
 CC
 SQ Sequence 1350 BP; 199 A; 489 C; 442 G; 220 T; 0 other;

Query Match 3.3%; Score 45; DB 23; Length 1350;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 292 TCGTCCATCGTGACCTGTGCGCCATCAGCTGAGCCGCTACTGG 336
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 DB 355 TCGTCCATCGTGACCTGTGCGCCATCAGCTGAGCCGCTACTGG 399

RESULT 15

ACAS6582
 ID ACAS6582 standard; cDNA; 3604 BP.
 AC ACAS6582;
 XX
 XX
 DT 06-JUN-2003 (first entry)
 XX
 DE Human signalling pathway polynucleotide probe SEQ ID NO 1180.
 XX
 KM Human; probe; se; array element; Parkinson's disease;
 KM signalling pathway population; cancer; adenocarcinoma; leukaemia;
 KM immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 XX
 OS Homo sapiens.
 XX
 PN U86500938-B1.
 XX
 PD 31-DEC-2002.
 XX
 PF 30-JAN-1998; 98US-0016434.
 XX
 PR 30-JAN-1998; 98US-0016434.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Au-Young J, Sellhammer JJ;
 DR WPI; 2003-352189/33.
 XX
 PT Combination of polynucleotide probes, useful as array elements in a
 PT microarray for monitoring the expression of a number of target
 PT polynucleotides -
 XX
 PS Claim 1; SEQ ID NO 1180; 65bp; English.
 XX
 CC The invention relates to a combination which, comprises a number of
 CC polynucleotide probes comprising a sequence selected from one of the 1490
 CC sequences mentioned in the specification. The combination is useful as an
 CC array element in a microarray for monitoring the expression of a number
 CC of target polynucleotides. The microarray is particularly useful in the
 CC diagnosis and treatment of cancer and immunopathology and neuropathology.
 CC The microarray is useful in diagnostic and treatment regimens, drug
 CC discovery and development, toxicological and carcinogenicity studies,
 CC forensics and pharmacogenomics. The microarray is also useful for
 CC monitoring progression of diseases and for developing sophisticated
 CC profiles for the effects of currently available therapeutic drugs. The
 CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
 CC and genomic fragments and in research and diagnostic applications. The
 CC array can detect changes in expression in a large number of genes coding
 CC for different signalling pathway populations which can be used to diagnose
 CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
 CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
 CC and Parkinson's disease. The present sequence represents a polynucleotide
 CC probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=06500938B1.
 CC
 XX
 SQ Sequence 3604 BP; 555 A; 1272 C; 1134 G; 643 T; 0 other;

Query Match 3.3%; Score 45; DB 25; Length 3604;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 292 TCGTCCATCGTGACCTGTGCGCCATCAGCTGAGCCGCTACTGG 336
 |||||
 DB 2432 TCGTCCATCGTGACCTGTGCGCCATCAGCTGAGCCGCTACTGG 2476

Search completed: February 8, 2004, 01:59:40
 Job time : 397.679 secs

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MEDIUM TYPE: Floppy disk

541 TTCTTTGCTCCTTGCATCATGATTCCTTGTCCTACCTGGCATCTCACTGATCGCCAAA 600
 953 TTCTTTGCTCCTTGCATCATGATTCCTTGTCCTACCTGGCATCTCACTGATCGCCAAA 1011

| | | | |
|----|------|--|------|
| QY | 601 | CGCAGCAACGCGACAGAGTCCCGAGGCGCCAAAGGGGGGGCTTGGGCAGGGGTAGATCCCAACAG | 660 |
| Db | 1013 | CGCAGCAACGCGACAGAGGTCCCGAGGCGCCAAAGGGGGGGGGCTTGGGCAGGGGTAGATCCCAACAG | 1072 |
| QY | 661 | CCCCGACCCGACCATGTGTGGGGCTTTGGGCTCAGCGAACTGCGACGCTTGCCCTCTGTG | 720 |
| Db | 1073 | CCCCGACCCGACCATGTGTGGGGCTTTGGGCTCAGCGAACTGCGACGCTTGCCCTCTGTG | 1132 |
| QY | 721 | GCTTCTGCAGAGAGGTCAACGGAACACTCGAAGTCACTGCGGAGAGAGAGAGAGGGGGAG | 780 |
| Db | 1133 | GCTTCTGCAGAGAGGTCAACGGAACACTCGAAGTCACTGCGGAGAGAGAGAGAGGGGGAG | 1192 |
| QY | 781 | ACCCCTGAAGATATCTGGGACCCGGGCTTTGGCCACCCAGTTGGGGCGGCCCTTCCCACTCA | 840 |
| Db | 1193 | ACCCCTGAAGATATCTGGGACCCGGGCTTTGGCCACCCAGTTGGGGCTTCCCTTCCCACTCA | 1252 |
| QY | 841 | GGCCAGGGCCAAAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG | 900 |
| Db | 1253 | GGCCAGGGCCAAAGAGGGGTGTTGTGGGGCATCTCCAGAGATGAAGCTGAAGAGAG | 1312 |
| QY | 901 | GA 902 | |
| Db | 1313 | GA 1314 | |

RESULT 2
 US-09-016-434-1180
 Sequence 1180, Application US/09016434
 Patent No. 6500938
 GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 APPLICANT: Jeffrey J. Sellmeyer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HERewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0002 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 1180:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3604 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GENBANK
 CLONE: g178195

| Query Match | 3.3% | Score 45 | DB 4 | Length 3604 |
|-----------------------|----------------|---|----------|-------------|
| Best Local Similarity | 100.0% | Pred. No. 4.9e-11 | | |
| Matches 45 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 292 | TCGTGCATTCGCGACCTGTGGCGCATAGCTGGAACGGCTACTG | 336 | |
| DB | 2432 | TCGTTCATCTGCACCTGTGGCGCATAGCTGGAACGGCTACTG | 2476 | |

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1      RESULT 3
2      US-09-016-434-1256
3      : Sequence 1256, Application US/09016434
4      : Patent No. 6500938
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Janice Au-Young
9      : APPLICANT: Jeffrey J. Seilhamer
10     : TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
11     : TITLE OF INVENTION: PATHWAY GENE EXPRESSION
12     : NUMBER OF SEQUENCES: 1490
13     : CORRESPONDENCE ADDRESS:
14     : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
15     : STREET: 3174 PORTER DRIVE
16     : CITY: PALO ALTO
17     : STATE: CALIFORNIA
18     : COUNTRY: USA
19     :
20     : ZIP: 94304
21     :
22     : COMPUTER READABLE FORM:
23     : MEDIUM TYPE: Floppy disk
24     : OPERATING SYSTEM: IBM PC compatible
25     : SOFTWARE: word Perfect 6.1 for windows/MS-DOS
26     :
27     : CURRENT APPLICATION DATA:
28     : APPLICATION NUMBER: US/09/016,434
29     : FILING DATE: HERewith
30     :
31     : CLASSIFICATION:
32     : PRIOR APPLICATION DATA:
33     : APPLICATION NUMBER:
34     : FILING DATE:
35     :
36     : CLASSIFICATION:
37     : ATTORNEY/AGENT INFORMATION:
38     : NAME: Zeller, Karen J.
39     : REGISTRATION NUMBER: 37,071
40     : REFERENCE/DOCKET NUMBER: PA-0002 US
41     : TELECOMMUNICATION INFORMATION:
42     : TELEPHONE: (650) 855-0555
43     : TELEFAX: (650) 845-4166
44     : INFORMATION FOR SEQ ID NO: 1256:
45     : SEQUENCE CHARACTERISTICS:
46     : LENGTH: 1382 base pairs
47     : TYPE: nucleic acid
48     : STRANDEDNESS: single
49     : TOPOLOGY: linear
50     : IMMEDIATE SOURCE:
51     : LIBRARY: GENBANK
52     : CLONE: G219405
53     :
54     : US-09-016-434-1256

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| | | | | |
|-----------------------|--------|-------------------------------------|------|--------------------------------|
| Query Match | 2.9% | Score 39 | DB 4 | Length 1382 |
| Best Local Similarity | 100.0% | Score 2,6e+08 | | |
| Matches | 39 | Conservative | 0 | Mismatches 0; Indels 0; Gaps 0 |
| QY | 1132 | GTGCTCTGCTGGTTCCTTCTTTGAGTCACAGCCTG | 1170 | |
| | | | | |
| | | | | |
| db | 1164 | GTGCTCTGCTGGTTCCTTCTTTGAGTCACAGCCTG | 1202 | |

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Search completed: February 8, 2004, 06:38:58
Job time : 89.703 secs
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US-09-016-434-1180

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2004, 01:25:52 ; Search time 313.58 Seconds
(without alignments)
10491.225 Million cell updates/sec

Title: US-09-692-077D-2

Perfect score: 1344

Sequence: 1 atggaccaccagagaccctca.....ggaccacagagcgtgtgta 1344

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 1215238056 residues

Word size : 30

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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1: em_estda:*
2: em_esthm:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
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14: gb_est5:*
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17: em_gse_hum:*
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19: em_gse_pln:*
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24: em_gse_pro:*
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26: em_gse_phg:*
27: em_gse_vtl:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 384 | 28.6 | 1044 | 13 | BQ880026 |
| 2 | 47 | 3.5 | 551 | 9 | A1169366 |
| 3 | 47 | 3.5 | 731 | 14 | CAS11027 |
| 4 | 45 | 3.3 | 2410 | 11 | BC035047 |

| 5 | 44 | 3.3 | 893 | 12 | BI459381 |
|----|----|-----|------|----|-----------|
| 6 | 41 | 3.1 | 872 | 29 | EC4A2BAR |
| 7 | 39 | 2.9 | 301 | 14 | T39448 |
| 8 | 39 | 2.9 | 978 | 13 | BUS39106 |
| 9 | 39 | 2.9 | 1031 | 13 | BUS38114 |
| 10 | 39 | 2.9 | 1176 | 9 | AL549866 |
| 11 | 39 | 2.9 | 1201 | 9 | AL573897 |
| 12 | 38 | 2.8 | 988 | 13 | BQ887729 |
| 13 | 34 | 2.5 | 683 | 12 | BG830756 |
| 14 | 34 | 2.5 | 855 | 29 | GC4A2AAR |
| 15 | 34 | 2.5 | 960 | 13 | BUS38113 |
| 16 | 34 | 2.5 | 967 | 29 | CNS03THX |
| 17 | 33 | 2.5 | 451 | 9 | AI461341 |
| 18 | 33 | 2.5 | 860 | 29 | CNS03HKO |
| 19 | 32 | 2.4 | 350 | 10 | BE648878 |
| 20 | 32 | 2.4 | 723 | 12 | BUS16840 |
| 21 | 32 | 2.4 | 761 | 14 | CB952602 |
| 22 | 32 | 2.4 | 3594 | 11 | AK046802 |
| 23 | 31 | 2.3 | 251 | 10 | BB603339 |
| 24 | 30 | 2.2 | 753 | 13 | BUS289357 |
| 25 | 30 | 2.2 | 836 | 13 | BU473325 |
| 26 | 30 | 2.2 | 1080 | 29 | CC240340 |

ALIGNMENTS

RESULT 1
BQ880026 1044 bp mRNA linear EST 16-AUG-2002
LOCUS AGENCOURT 8113358 Lupeki dorsal root ganglion Homo sapiens cDNA
DEFINITION clone IMAGE:6179035 5', mRNA sequence.
ACCESSION BQ880026
VERSION BQ880026.1 GI:22272034
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1044)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.femail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM13559 row: 1 column: 20
High quality sequence stop: 430.

FEATURES

source

1. 1044
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6179035"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupeki dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCGACGCTCC-3' and
5'-GACTACTTCTAGATCGGACGCGCCCTT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drl)8 tail. The sequence tag for this library is CATCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

BASE COUNT 128 a 217 c 163 g 223 t

Query Match 3.5%; Score 47; DB 14; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 CATGGCTCTTCAGTCTCTCTGTGATGGCTACTGCAAGCTC 1250
DB 42 CATGGCTCTTCAGTCTCTCTGTGATGGCTACTGCAAGCTC 88

RESULT 4 BC035047 2410 bp mRNA linear HTC 23-SEP-2002
LOCUS BC035047 Homo sapiens, similar to adrenergic, alpha-2A-, receptor, clone
IMAGE:5266354, mRNA.
ACCESSION BC035047
VERSION BC035047.1 GI:23272892
KEYWORDS HTC.
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 2410)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshituki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 73 Row: 0 Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15718669
This clone has the following problem: frame shifted.

FEATURES Location/Qualifiers

source 1..2410

BASE COUNT 406 a 813 c 721 g 470 t
ORIGIN
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5266354"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/note="Vector: pBluescript"

Query Match 3.3%; Score 45; DB 11; Length 2410;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TCGTCATCGTGACCTGTGGCCATCAGCGCTGAGCGTACTGG 336
DB 568 TCGTCATCGTGACCTGTGGCCATCAGCGCTGAGCGTACTGG 612

RESULT 5 BI459381 893 bp mRNA linear EST 21-AUG-2001
LOCUS BI459381
DEFINITION 603200147F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5266354 5', mRNA sequence.
ACCESSION BI459381
VERSION BI459381.1 GI:15250037
KEYWORDS EST.
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 893)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC <http://mgc.nci.nih.gov/>
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshituki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Plate: LLM11671 row: m column: 11
High quality sequence stop: 716.
Location/Qualifiers

FEATURES source 1..893

BASE COUNT 149 a 303 c 290 g 151 t
ORIGIN
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5266354"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTATTTTATTTTAA-3', size-selected for average insert size 2.2 kb and normalized to 10⁷ 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

Query Match 3.3%; Score 44; DB 12; Length 893;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 CGTCATCGTGACCTGTGGCCATCAGCGCTGAGCGTACTGG 336
DB 574 CGTCATCGTGACCTGTGGCCATCAGCGCTGAGCGTACTGG 617

RESULT 6 ECAA2BAR 872 bp DNA linear GSS 14-SEP-2001
LOCUS ECAA2BAR
DEFINITION Horse alpha2 adrenergic receptor gene fragment probably subtype b, genomic survey sequence.
ACCESSION AL606560
VERSION AL606560.1 GI:15591917
KEYWORDS GSS; Alpha2 adrenergic receptor gene.
SOURCE Equus caballus (horse)

[illegible]

RESULT 9
BUS38114 1031 bp mRNA linear EST 13-SEP-2002
LOCUS
DEFINITION AGENCOURT 10186636 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6586828 5', mRNA sequence.
BUS38114
ACCESSION
VERSION BUS38114.1 GI:22848555
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1031)
TITLE NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rmail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
plate: LICM2754 row: j column: 20
High quality sequence, stop: 529.
Location/Qualifiers
1. 1031
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6586828"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_idb="NIH MGC 107"
/note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT 221 a 275 c 330 g 191 t 14 others
ORIGIN
Query Match 2.9%; Score 39; DB 13; Length 1031;
Best Local Similarity 100.0%; Pred. No. 7.8e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1132 GTGCTGTGCTGTTCCCTTCTTTCAGCTACAGCCTG 1170
|||||
Db 12 GTGCTGTGCTGTTCCCTTCTTTCAGCTACAGCCTG 50
|||||
RESULT 10
AL549866 1176 bp mRNA linear EST 31-MAY-2003
LOCUS
DEFINITION AL549866 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1054YH02 5-PRIME, mRNA sequence.
AL549866
ACCESSION
VERSION AL549866.2 GI:31271684
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1176)
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished

COMMENT
On Feb 15, 2001 this sequence version replaced gi:12886265.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue Genoscope sequence ID : CSOD1054D010P1.
Location/Qualifiers
1. 1176
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1054YH02"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_idb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 194 a 338 c 425 g 174 t 45 others
ORIGIN
Query Match 2.9%; Score 39; DB 9; Length 1176;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1132 GTGCTGTGCTGTTCCCTTCTTTCAGCTACAGCCTG 1170
|||||
Db 552 GTGCTGTGCTGTTCCCTTCTTTCAGCTACAGCCTG 590
|||||
RESULT 11
AL573897 1201 bp mRNA linear EST 31-MAY-2003
LOCUS
DEFINITION AL573897 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1054YH02 3-PRIME, mRNA sequence.
AL573897
ACCESSION
VERSION AL573897.2 GI:31295233
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1201)
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
On Feb 16, 2001 this sequence version replaced gi:12933576.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue Genoscope sequence ID : CSOD1054D010P1.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1054YH02"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_idb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 193 a 391 c 364 g 205 t 48 others
ORIGIN

Query Match 2.9%; Score 39; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred. No. 8e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 GTGCTGCGGTTCCCTCTCTCTGAGTACAGCCTG 1170
|||||
DB 733 GTGCTGCGGTTCCCTCTCTCTGAGTACAGCCTG 695

RESULT 12

BO887729 988 bp mRNA linear EST 16-AUG-2002
LOCUS BO887729
DEFINITION AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
5', mRNA sequence.
BO887729
BO887729.1 GI:22279743
EST.
SOURCE Mus musculus (house mouse)

ACCESSION

BO887729
BO887729
BO887729.1 GI:22279743
EST.
SOURCE Mus musculus (house mouse)

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 13

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 683)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

QY 1217 AGTTCTTCTCTGATCGGCTACTGCAACGCTC 1250
|||||
DB 100 AGTTCTTCTCTGATCGGCTACTGCAACGCTC 133

REFERENCE

BO887729 988 bp mRNA linear EST 16-AUG-2002
LOCUS BO887729
DEFINITION AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
5', mRNA sequence.
BO887729
BO887729.1 GI:22279743
EST.
SOURCE Mus musculus (house mouse)

ACCESSION

BO887729
BO887729
BO887729.1 GI:22279743
EST.
SOURCE Mus musculus (house mouse)

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 14

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 683)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

QY 1217 AGTTCTTCTCTGATCGGCTACTGCAACGCTC 1250
|||||
DB 100 AGTTCTTCTCTGATCGGCTACTGCAACGCTC 133

REFERENCE

BO887729 988 bp mRNA linear EST 16-AUG-2002
LOCUS BO887729
DEFINITION AGENCOURT_8764335 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313133
5', mRNA sequence.
BO887729
BO887729.1 GI:22279743
EST.
SOURCE Mus musculus (house mouse)

ACCESSION

BO887729
BO887729
BO887729.1 GI:22279743
EST.
SOURCE Mus musculus (house mouse)

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

RESULT 14

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BASE COUNT 201 a 248 c 245 g 161 t
ORIGIN

Query Match 2.5%; Score 34; DB 29; Length 855;
Best Local Similarity 100.0%; Pred.No. 0.00016;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 366 CAAGCCACCCCGCCGATCAAGTCATCATC 399
DB 144 CAAGCCACCCCGCCGATCAAGTCATCATC 177

RESULT 15
BU538113 960 bp mRNA linear EST 13-SEP-2002
LOCUS AGENCOURT 10186620 NIH_MGC_107 Homo sapiens CDNA clone
DEFINITION IMAGE:6568627 5', mRNA sequence.
ACCESSION BU538113
VERSION BU538113.1 GI:22848554
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 960)
JOURNAL NIH-MGC http://mgs.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2754 row: j column: 19
High quality sequence start: 46
High quality sequence stop: 558.
Location/Qualifiers

FEATURES
source
1. 960
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6568627"
/cissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 107"
/note="Organ: breast; Vector: pORF7; Site_1: EcoRI;
Site_2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT 214 a 268 c 294 g 184 t
ORIGIN

Query Match 2.5%; Score 34; DB 13; Length 960;
Best Local Similarity 100.0%; Pred.No. 0.00016;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1217 AGTTCTTCTTGATCGGCTACTGCAACAGCTC 1250
DB 97 AGTTCTTCTTGATCGGCTACTGCAACAGCTC 130

Search completed: February 8, 2004, 06:35:53
Job time : 3115.58 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:44:02 ; Search time 5085.47 Seconds

(without alignments)
10811.687 Million cell updates/sec

Title: US-09-692-077D-2

1344

Sequence: 1 atgaccaccagagccctta.....ggaccacagagcctgctga 1344

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_hy:*
39: em_hygo_hum:*
40: em_hygo_mus:*
41: em_hygo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1344 | 100.0 | 1344 | 6 | AX350490 |
| 2 | 1344 | 100.0 | 1344 | 9 | AF315895 |
| 3 | 1340.8 | 99.8 | 22842 | 9 | AC092603 |
| 4 | 1325 | 98.6 | 1353 | 6 | AX350489 |
| 5 | 1325 | 98.6 | 9842 | 6 | AF005900 |
| 6 | 1321.8 | 98.3 | 2072 | 6 | AR270618 |
| 7 | 1321.8 | 98.3 | 2072 | 6 | HUMADRA2RA |
| 8 | 1321.8 | 98.3 | 3274 | 6 | AX548756 |
| 9 | 1132.8 | 84.3 | 1356 | 4 | AF150333 |
| 10 | 1046 | 77.8 | 1987 | 10 | CP025723 |
| 11 | 1007.8 | 75.0 | 6268 | 10 | AF366899 |
| 12 | 1007.8 | 75.0 | 124474 | 2 | AC126878 |
| 13 | 1006.6 | 74.9 | 1639 | 10 | RNA2BARA |
| 14 | 1003 | 74.6 | 2319 | 10 | RAT2BR |
| 15 | 996.8 | 74.2 | 276543 | 2 | AC112830 |
| 16 | 995 | 74.0 | 1347 | 10 | AF332049 |
| 17 | 995 | 74.0 | 1650 | 10 | MUSADRENH |
| 18 | 993.4 | 73.9 | 1347 | 10 | AF332050 |
| 19 | 993.4 | 73.9 | 83802 | 10 | AL731836 |
| 20 | 986.4 | 73.4 | 1180 | 9 | NC0251186 |
| 21 | 977.4 | 72.7 | 9377 | 10 | MUSADRECA |
| 22 | 974.4 | 72.5 | 1171 | 9 | CVA251182 |
| 23 | 970 | 72.2 | 1168 | 4 | TTA251187 |
| 24 | 967.8 | 72.0 | 1180 | 4 | LPA505821 |
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Sequence 2 from Patent WO0179561.
ACCESSION AX350490
VERSION AX350490.1 GI:18616092
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 2 25-Oct-2001.

Pred. No. 1s the number of results predicted by chance to have a

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| Query Match | 100.0%; | Score 1344; | DB 6; | Length 1344; |
| Best Local Similarity | 100.0%; | Pred. No. | 7e-216; | |
| Matches 1344; | Conservative | 0. | Mismatch | 1 |

[illegible]

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| LOCUS | AF316895 | | | | gene, complete |
| DEFINITION | Homo sapiens alpha 2B adrenergic receptor (ADRA2B) | | | | |
| ACCESSION | AF316895 | | | | |
| VERSION | AF316895.1 | | | | |
| KEYWORDS | | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| AUTHORS | 1 (bases 1 to 1344) | | | | |
| TITLE | Small,K.M., Brown,K.M., Forbes,S.L. and Liggett,S.B. | | | | |
| JOURNAL | Polymorphic deletion of three intracellular acidic residues of the alpha 2B-adrenergic receptor decreases G protein-coupled receptor kinase-mediated phosphorylation and desensitization | | | | |
| REFERENCE | J. Biol. Chem. 276 (7), 4917-4922 (2001) | | | | |
| PMID | 11056163 | | | | |
| AUTHORS | 2 (bases 1 to 1344) | | | | |
| TITLE | Small,K.M., Brown,K.M., Forbes,S.L. and Liggett,S.B. | | | | |
| JOURNAL | Direct Submission | | | | |
| FEATURES | Submitted (26-OCT-2000) Internal Medicine, University of Cincinnati, 231 Bethesda Ave, Cincinnati, OH 45267, USA | | | | |
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Best Local Similarity 100.0%; Pred. No. 7e-216;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
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DEFINITION Homo sapiens BAC clone RP11-13946 from 2, complete sequence.
ACCESSION AC092603 AC073396
VERSION AC092603.2 GI:16303539
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 22842)
AUTHORS Sulistion, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 22842)
AUTHORS Martinka, S., Abbott, A., Hawkins, M., Elliott, G. and Doeber, A.
TITLE The sequence of Homo sapiens BAC clone RP11-13946
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 22842)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2001) Genome Sequencing Center, Washington
REFERENCE University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 22842)

AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
AUTHORS 5 (bases 1 to 22842)
TITLE Waterston,R.H.
JOURNAL Direct Submission
 Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 22842)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Oct 20, 2001 this sequence version replaced gi:14916188.

COMMENT

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: sapiens@wustl.wustl.edu
 Summary Statistics
 Center project name: H_NH0139J06
 Drafting Center: WIBR_NH0139J06

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateo,M., Caranese,J.V. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-401C13, 2000 bp overlap; the clone sequenced to the right is RP11-574017, 2000 bp overlap. Actual end of this clone is at base position 48999 of RP11-574017. Polymorphisms have been identified between AC013272 and AC092603.

The sequence of AC073396 has been incorporated into AC092603.

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VERSION   AX350489.1 GI:18616091
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          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Liggett, S.B. and Small, K.M.
  Alpha-2 adrenergic receptor polymorphisms
  Patient: WO 0179561-A.1 25-Oct-2001.
  Liggett, Stephen B. (US) ; Small, Kersten M. (US)
  Location/Qualifiers
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BASE COUNT      224 a 458 c 405 g 266 t
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Query Match      98.6%; Score 1325; DB 6; Length 1353;
Best Local Similarity 99.3%; Pred. No. 1.1e-212;
Matches 1344; Conservative 0; Mismatches 0; Indels 9; Gaps 1;
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 complete cds.
 ACCESSION AF005900
 VERSION AF005900.1 GI:2245627
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE
 1 (bases 1 to 9842)
 AUTHORS Cayla, C., Schack, S., Bouloumie, A., Dovedjian, J.C. and Paris, H.
 TITLE Alpha2C2-adrenergic receptor gene
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 9842)
 AUTHORS Cayla, C., Schack, S., Bouloumie, A., Dovedjian, J.C. and Paris, H.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,
 CHU Rangueil, Toulouse 31403, France

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DB 833 GCCGTATCTGCTGCGCGCGCATGATGATCATCTCTGATGAGCTCATGCC 892
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QY 541 TTCTTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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QY 661 CCCGACCCGACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 1073 CCCGACCCGACCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1132
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RESULT 8
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LOCUS AX548756 3274 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 41 from Patent WO02061087.
ACCESSION AX548756
VERSION AX548756.1 GI:25813686
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Burner, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
LOCATION/Qualifiers
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Best Local Similarity 99.2%; Pred. No. 3.3e-212;
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Db 721 CTGGCTACGCGGAGAGGCAATGGCACTCCAGCTCTCTGGGAAACAGGAGACGGG 780
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RESULT 10
CPUS5723 1987 bp DNA linear ROD 05-SEP-2001
LOCUS Cavia porcellus alpha-2B adrenoceptor gene, complete cds.
ACCESSION U55723.1 GI:818876
VERSION U55723.1 GI:818876
KEYWORDS
SOURCE
ORGANISM Cavia porcellus (domestic guinea pig)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
1 (bases 1 to 1987)
Svensson,S.B., Bailey,T.J., Porter,A.C., Richman,J.G. and
Regan,J.W.
Heterologous expression of the cloned guinea pig alpha 2A, alpha
2B, and alpha 2C adrenoceptor subtypes. Radioligand binding and
functional coupling to a CAMP-responsive reporter gene
Biochem. Pharmacol. 51 (3), 291-300 (1996)
JOURNAL MEDLINE 96152573
PUBMED 8573196
2 (bases 1 to 1987)
Richman,J.G.
Direct Submision
Submitted (26-APR-1995) Jeremy G. Richman, University of Arizona,
Pharmacology and Toxicology, College of Pharmacy, Room 235, Tucson,
AZ 85721, USA
FEATURES
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BASE COUNT 318 a 663 c 605 g 401 t
ORIGIN

Query Match 77.8%; Score 1046; DB 10; Length 1987;
Best Local Similarity 87.5%; Pred. No. 6.9e-166;
Matches 1181; Conservative 0; Mismatches 160; Indels 9; Gaps 3;

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RESULT 11
AP366899 6268 bp DNA linear ROD 15-MAY-2001
LOCUS Rattus norvegicus alpha2b-adrenergic receptor (Rng) gene, complete
DEFINITION cds.
ACCESSION AP366899 GI:14039788
VERSION AP366899
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus, Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM Eukaryota; Metazoa; Rodentia; Sclurognathu; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 6268)
AUTHORS Schack, S., Cussac, D. and Paris, H.
TITLES Cloning and characterization of the rat alpha2b-adrenergic receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6268)
AUTHORS Schack, S., Cussac, D. and Paris, H.
TITLES Direct Submision
JOURNAL Submitted (29-MAR-2001) U388, INSERM, CHU Rangueil, Toulouse 31403,
France
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Best Local Similarity 84.8%; Pred. No. 1.5e-159; Indels 3; Gaps 1;
Matches 1142; Conservative 0; Mismatches 202;
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Qy 61 TTCCTCATCTCTTACATCTTGGGCAACCTCGTGCATCTGCTGTGTACCAAC 2914
Db 2855 TTCCTCATCTCTTACATCTTGGGCAACCTCGTGCATCTGCTGTGTACCAAC 2914
Qy 121 CGCTGCTGCGCCCTCAGAACCTGTCGTGTGCTGCGCCGCGCGCATCTCTG 180
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Qy 181 GTGGCAAGCTCATCATCTCTTCTGCTGGGCAACAGAGCTGAGCTGACTGTTTC 3034
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Qy 241 CGGCGCAAGTGTGAGGTGATCTGCGCTGAGCTGCTTCTTGCACCTGTCATC 3094
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Qy 481 GCGCGCGAGTGAAGTCAACAGAGAGCGCTGATCATCTGCTTCAAGATCGATCT 540

contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GZCB
Center clone name: CH230-263M16

----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 114750 bases at least Q40
Consensus quality: 115674 bases at least Q30
Consensus quality: 116260 bases at least Q20
Estimated insert size: 117568; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 53390: contig of 53390 bp in length
* 53391 53490: gap of unknown length
* 53491 124474: contig of 70984 bp in length.
Location/Qualifiers

FEATURES

source

1. 124474

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-263M16"

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/note="clone_boundary"

clone_end:T7

site:

end_sequence:BZ271225"

43942..45204

/note="wgs_contig"

51753..53390

/note="wgs_contig"

complement(62624..63503)

/note="clone_boundary"

clone_end:Sp6

site:

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119922..122663

/note="wgs_end_extension"

clone_end:Sp6"

122714..124474

/note="wgs_end_extension"

clone_end:Sp6"

misc_feature

122714..124474

BASE COUNT 28445 a 29524 c 29014 g 29673 t 7818 others

ORIGIN

Query Match

75.0%; Score 1007.8; DB 2; Length 124474;

Best local Similarity

84.8%; Pred. No. 9.8e-160;

Matches 1142; Conservative

0; Mismatches 202; Indels 3; Gaps 1;

QY

1 ATGAGCAGCAGGAGCCCTACTCGTGAGGCCACAGGCGCATAGGCGCGCATAC 60

Db

57504 ATGAGCAGCAGGAGCCCTACTCGTGAGGCCACAGGCGCATAGGCGCGCATAC 57563

QY

61 TTCTCATTTCTTTACCATCTTGAGCAAGCTCTGATCATCTGGCTGTGTGACAG 120

Db

57564 TTCTCATTTCTTTACCATCTTGAGCAAGCTCTGATCATCTGGCTGTGTGACAG 57623

QY 1198 GTGCCCCAGTGGCTCTTCACAGTTCTTCTTGATCGGCTACTGCAACAGCTCACTGAC 1257
Db 58704 GTACCGCATGGCCCTTCCAGTTCTTCTTGATCGGCTACTGCAACAGCTCTTTGAAC 58763
QY 1258 CCTGTATCTTACACCATCTTCAACAGGACTTCGCGCTGCTTCCGAGAGATCTGTGC 1317
Db 58764 CCTGTATCTTACACCGCTTCAACAGGACTTCGCGCTGCTTCCGAGAGATCTTTGC 58823
QY 1318 CGCGCGTGACCGACGCGCTGTGA 1344
Db 58824 CGCGCTTGACCGACGCTGTGA 58850
RESULT 13
RNA2BARA 1639 bp DNA linear ROD 09-AUG-1995
LOCUS R.norvegicus gene for alpha-2B-adrenergic receptor.
DEFINITION X74400.1 GI:840862
ACCESSION alpha-2B-adrenergic receptor; epinephrine-binding; G-protein
KEYWORDS coupled receptor; norepinephrine-binding; transmembrane receptor.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Le Joesec, M., Cloix, J. F., Pecquery, R., Giudicelli, Y. and
Dausse, J. P.
TITLE Differential sodium regulation between salt-sensitive and
salt-resistant Sabra rats is not due to any mutation in the renal
alpha 2B-adrenoceptor gene
JOURNAL Am J Hypertens. 8 (2), 177-182 (1995)
MEDLINE 95275492
PUBMED 7755946
REFERENCE 2 (bases 1 to 1639)
AUTHORS Le Joesec, M. M.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1993) M. M. Le Joesec, Groupe de Signalisation,
Service de Biochimie, Paris-Ouest, 45 rue des Saintes Peres, 75270
Paris cedex 06, FRANCE
REMARK sequence revised by author 09-SEP-1993
COMMENT Related sequence: M32061.
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/sub_species="Sabra rats (SBH, SBN)"
/db_xref="taxon:10116"
/cfeature_type="renal"
178..1524
/codon_start=1
/product="alpha-2B-adrenergic receptor"
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/db_xref="GI:940816"
/db_xref="SWISS-PROT:P19328"
/translation="MDQEPYSVQATAAISATITPILITFISNALVILAVLTSRLR
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LPQCEINQAMVLIASSIGSFAPCLIMILIVYRIYIARSHRGAGXDRGEGS
KKQPVAGVPTSAKVPTLVSPLSVGANGHPKPREXEGTPEDPARALPTWS
ALPRSGQCKKGTSGATABEGXEDBEVBECEPQLPASPVCNPIQOPTSRVL
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Db 178 ATGACCATCAAGAGCCCTACTGCGTGACAGCCACCGCCCATCGGCTGAGCATCACC 237
QY 61 TTCCATTTCTTTTACATCTTGGGAAGCTCTGGTATCCGAGCTGATGACAGC 120
Db 238 TTTCATCTTTTACCATTTTGGCATTCGCTGGTATCTTGGTGTGACAGC 297
QY 121 CGCTCGTGGCCGCCCTCAGAACCTGTTCTGATGCTGCTGCGCCGCGCAGATCTG 180
Db 298 CGTCACTCGGTACACCAAAACCTGTTCTGATGCTGCTGCGAGAGCGACATCTTA 357
QY 181 GTGGCAAGCTCATCATCTTTTCTGCTGCGCAAGAGCTGCGGACTACTGACTTC 240
Db 358 GTGGTACTCTCATCATCTTTTCTGCTGCGCAAGAGCTGCGGCTGCTGCTGCTT 417
QY 241 CGGCGACGCTGCGAGGCTGCTGCGCTGAGTGTCTTCTGCACTCTGCTCATC 300
Db 418 TGGCGGCGGTGGCGAGGTCTACCTGGCGCTAGAGTGTCTTCTGATCTTCTCATC 477
QY 301 GTGCACCTGCGCCCATCAGACCTGACCCGCTACTGGGCGCTGAGCCGCGCTGAGTAC 360
Db 478 GTGCACCTGCTGCTCATCAGCTGACAGAGTACTGGGCGAGTACCGAGATGGAGTAC 537
QY 361 AACTCAAGGCAACCCGCGCGCATCAAGTGCATCTCTGCTGCTCATGCC 420
Db 538 AACTCAAGGCACTCGCGCGCATCAAGTGCATCTCTGCTGCTCATGCA 597
QY 421 GCGGTATCTGCTGCGCGCGCATCTCAAGGCGCAAGGCGCGCGCGCGCGCG 480
Db 598 GCTGTATTTCTTACCGCGCGCATCTCAAGGCGCAAGGCGCGCGCGCGCG 657
QY 481 CGCCCGCAGTGAAGCTCAACAGAGGCTGTATACCTGCTGCTGCTGCTGCTGCT 540
Db 658 CTCCCGCAGTGAAGCTCAACAGAGGCTGTATACCTGCTGCTGCTGCTGCTGCT 717
QY 541 TTCTTGTCTCTTCTCTCATCATGATCTTGTCTACCTGCGCATCTCATCGCAAA 600
Db 718 TTTTGTCTCTCTCTCTCATCATGATCTTGTCTACCTGCGCATCTCATCGCAAA 777
QY 601 CGCAGCAACCGCAGAGTCCAGAGGCGCGCGCGCTGAGGAGGTAGTCAAGCAG 660
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QY 661 CCGCAGCCGCAAGTGTGGGCTTGGCTGCGCAACCTGCGAGCCCTGCTGCTGCT 717
Db 838 CCGCAGCCGCTGTGCTGCGGAGTCCAGCTTCAAGTGTGCGCACTGCTGCTGCT 897
QY 718 GTGCTTCTGCGCAGAGGTCAACGCACTCGAAGTCACTGCGGAGAGAGAGAGG 777
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QY 778 GAGACCTCTGAGATCTGAGGACCCGCGCTTGCACCCAGTGGGCTGCTTCCCAAC 837
Db 958 GAGACCTCTGAGATCTGAGGACCCGCGCTTGCACCCAGTGGGCTGCTTCCCAAC 1017
QY 838 TCAAGCGAGGCGCAGAGAGGCTGTTGTGGGCGCATCTCGAGAGATGAAGTGAAG 897
Db 1018 TCAAGCGAGGCGCAGAGAGGCTGTTGTGGGCGCATCTCGAGAGATGAAGTGAAG 1077
QY 898 GAGAGAGAGAGAGAGAGTGAACCCAGGCGAGTGTCTCGGCTGAGTCAAGCT 957
Db 1078 GAGAGAGAGAGAGAGATGAAGTGAACCCAGGCGAGTGTCTCGGCTGAGTCAAGCT 1137
QY 958 TGAAGCCCCCGCTGCAAGCAGCAGGCTCCGCGTGTGCGCACCTGAGTGCAG 1017
Db 1138 TGAAGCCCCCGCTGCAAGCAGCAGGCTCCGCGTGTGCGCACCTGAGTGCAG 1197
QY 1018 GTGCTCTGCGGCGAGGCGGTGCTATAGTGGGCGAGTGTGGAGAGGCGCGAG 1077
Db 1198 GTGCTCTGCGGCGAGATGGAGTGGAGTGGCGAGTGGCGAGAGGCGCGAG 1257
QY 1078 CTGACCCGAGAGAGGCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137
Db 1258 CTGACCCGAGAGAGGCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317

| | | | |
|----|------|---|------|
| Oy | 1138 | GGCGGGTCCCCCTTTCTTCAAGCTACAGCCTGGGCGCCATCTGCCGAGACCTGGCAAG | 1197 |
| Db | 1318 | TGCTGGTTCTTTCTTTCTTCAAGCTACAGCCTGGGGGGCCATCTGCCACACACTGGCAAG | 1377 |
| Oy | 1198 | GTGCCCATGAGCGCTTTCACAGTTCTTCTTGGATCGGCTACTGCAACAGCTCACTGAAC | 1257 |
| Db | 1378 | GTACCGCATGGCGCTTTCACAGTTCTTCTTGGATCGGCTACTGCAACAGCTCTTTGAAC | 1437 |
| Oy | 1258 | CCTGTTATCTACACCATTTTCAACACGAGACTTTCGGCGGTGCTTTCGGAGGATCCTGTGC | 1317 |
| Db | 1438 | CCTGTCATCTACACCGTCTTCAACACGAGACTTTCGGCGGTGCTTTCGAAGATCCTTTGC | 1497 |
| Oy | 1318 | CGCCCGTGGACCCAGACGGCGCTGGTGA | 1344 |
| Db | 1498 | CGCCCGTGGACCCAGACTGGCGTGGTGA | 1524 |

RESULT 14

| | | | | | |
|------------|--|-----------|---------------------|--------|----------------|
| LOCUS | RAT2B9 | 2319 bp | mRNA | linear | ROD 27-MR-1993 |
| DEFINITION | Rat alpha-2B-adrenergic receptor (RNG-alpha-2) | | mRNA, complete cds. | | |
| ACCESSION | M32061 | | | | |
| VERSION | M32061.1 | GI:202589 | | | |
| KEYWORDS | adrenergic receptor. | | | | |
| SOURCE | Rattus norvegicus (Norway rat) | | | | |
| ORGANISM | Rattus norvegicus | | | | |

| | |
|-----------|--|
| REFERENCE | (bases 1 to 2319) |
| AUTHORS | Zeng, D.W., Harrison, J.K., D'Angelo, D.D., Barber, C.M., Tucker, A.L., Lu, Z.H. and Lynch, K.R. |
| TITLE | Molecular characterization of a rat alpha 2B-adrenergic receptor |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. 87 (8), 3102-3106 (1990) |
| MEDLINE | 90222177 |
| PUBMED | 2158103 |
| COMMENT | Original source text: Rat (strain Sprague Dawley) adult kidney. |

Draft entry and computer-readable sequence [1] kindly submitted by K.R. Lynch, 12-FEB-1990.

| FEATURES | Location/Qualifiers |
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| source | 1..2319 |
| | /organism="Rattus norvegicus" |
| | /mol_type="mRNA" |
| | /strain="Sprague-Dawley" |
| | /db_xref="taxon:10116" |
| | /sex="male" |
| | /tissue_type="kidney" |
| | /dev_stage="adult" |
| gene | 1..2319 |
| | /gene="RNG-alpha-2" |
| CDS | 366..1727 |

| BASE COUNT | a | c | g | t |
|------------|-----|-----|-----|-----|
| ORIGIN | 433 | 700 | 618 | 568 |

Query Match

74.68; Score 1003; DB 10; Length 2319;

Best Local Similarity 84.6%; Pred. No. 1.1e-158;
Matches 1139; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

| | | |
|----|---|------|
| QY | ATGAGACCAACAGAGACCCCTACCTCCGTCAGAGGACACAGCGGCCATAGCGCGGCATCACCC | 60 |
| Db | ATGAGACCAACAGAGACCCCTACCTCCGTCAGAGGACACAGCGGCCATAGCGCGGCATCACCC | 381 |
| QY | TTCTCATTTCTCTTAACTTCTTGGACAAGCTCTGTGCATCTCGAGTCTGTGTGACAGC | 120 |
| Db | TTTTCATCTCTTTTCAACCATTTTTCGCAATGGCGTGGTCAATCTCGAGTGTGTGTGACAGC | 441 |
| QY | CGCTCGCGCGCGGCCCTTCAGAACCTGTGTTCTGTGTGTGGCTGTGGCGCGCGGCATCTCTG | 180 |
| Db | CGCTCACTCCGTCACCAACAAAACCTGTTCCTGTGTGTCACTGGCAGACGCCACATCTCTA | 501 |
| QY | GTGGCCACGCTCATATCCCTTTCTCGGTGGCCAAAGAGCTGTGGGCTAATGTGATCTTC | 240 |
| Db | GTGGCTACTCTCATATCCCTTTCTCTGTGGCAACAGAGCTGTGGGCTAATGTGATCTTC | 561 |
| QY | CGGCGCACTGTGTGTGGAGTGTACTCTGGCGCTCGAGCTGTCTTGTGCACTCTCTGCATC | 300 |
| Db | TGGCGTGTGTGTGTGAGGTCTTACCTGTGGCGCTTACAGCTGTCTTGTATCTCTCTCCATC | 621 |
| QY | GTGCACCTGTGGCGCATAGCGCTGTGACCGCTACTGTGGCGCGTGTGAGCGCGCTGTGAGTAC | 360 |
| Db | GTGCACCTGTGTGGCATAGCGCTGTGACCGCTACTGTGGCGCGTGTGAGCGCGCTGTGAGTAC | 681 |
| QY | AACTCCAAAGCGCACCCCGCGCGCATCAAGTGCATATCTTCACTGTGTGCTCATCGCC | 420 |
| Db | AACTCCAAAGCGCACCCCGCGCGCATCAAGTGCATATCTTCACTGTGTGCTCATCTTCA | 741 |
| QY | GCGGTCACTGTGGCTGCGCGCCCTCATATCAAAAGGCGACAGAGGCGCCCAAGCGCGCGGG | 480 |
| Db | GCTGTCAATTTCTTACCGCCCTCATATCTTCAAGGGCGACCAAGCGCCCGAGCGCGGG | 801 |
| QY | CGCCCCCACTGCAAGCTCAACACAGAGGCGTGTGATCATCTGTGGCTCTCAGCATCGGATCT | 540 |
| Db | CTCCCCCACTGTGAGCTCAACACAGAGGCGCTGTGATCATCTTGGCTTCAGCATCGGATCT | 861 |
| QY | TTCTTTGTCTCTGTGCTCATATATGCTTGTCTTACCTGTGGCATCTTACCTGTATCGCCAAA | 600 |
| Db | TTTTTTGTCTCTGTGCTCATATATGCTTGTCTTACCTGTGCAATCTAAGTATGTCCAAA | 921 |
| QY | CGACGCAACCGCAGAGGTCCCAAGGCGCAAGGGGGGGCTGTGGCAGGGTGAATCCAAAGCAG | 660 |
| Db | CGACGCACTGTGCAAGGTCTGTGAGCCAAAGGGGGCTGTGGAGAAAGGTGAATCCAAAGAG | 981 |
| QY | CCCCGACCCGACATGTGTGGGGCTTTTGGCTCAAGCCAAATCTGCCAGCTTGTGGCT--CT | 717 |
| Db | CCCCAGCCGGTGTGTGGGGAGTGCACCTTCAAGCTTAAAGTGTGCCACCTGTGTCTCTCT | 1041 |
| QY | GTGGCTTCTGTCCAGAGAGTCAACGGAACACTCGAAGTCCACTGTGGGAGAAAGAGAGAGGG | 777 |
| Db | CTATCTTCTGTGTGAGAGGCCAATGGACACCCCAAGGCTCCAAAGAGAGAGAGAGAGGGG | 1101 |
| QY | GAGACCCCTTGAAGTCTGTGAGGCCAGGGCTTTTGGCCCAACTTGTGTGCCCTTCCAGA | 1220 |
| Db | GAGACCCCTTGAAGTCTGTGAGGCCAGGGCTTTTGGCCCAACTTGTGTGCCCTTCCAGA | 1161 |
| QY | TCAGGCCAGGGCCAGAAAGAGGGTGTGTGTGGGGCATCTCCAGAGATGTGAAGCTGAAGAG | 897 |
| Db | TCAGGCCAAGGCCAGAAAGAGGGGACTAAGTGTGGGCCATCTCCAGAGAGAGAGATGAAGAG | 1221 |
| QY | GAGAGAGAGAGAGAGAGAGTGTGAACCCCAAGGCAAGTGCAGAGTCTCTCGGCTCTCAGT | 957 |
| Db | GATGAGGAAAGGTGTGAAGATGTGAACCCCAACACTGCACACATCTCTGTGCTCGGTGA | 1281 |
| QY | TGCAGCCCGCCGCTGTGACAGCCACAGAGGCTCCCGGGTGTGGCAACCTTACGTGGCGAG | 1017 |
| Db | TGCACCCCACTTGTGACAGCGCTCAGACTTCTCTCGGGTACTTGGCCACACTTCTGTGGCGAG | 1341 |
| QY | GTGCTCTCTGGGCAAGGGCGTGGGTGCTTATTAAGTGTGGCAAGTGTGGCGCTGCAGAGGGCGAG | 1077 |
| Db | GTGCTCTCTGGGCAAGGGCGTGGGTGCTTATTAAGTGTGGCAAGTGTGGCGCTGCAGAGGGCGAG | 1018 |

Db 1401 GTGCTTCTGGGCAAGAAATGTGGAGTTGCCAGATGGGCGACAGTGGCCGACGACAG 1460

Qy 1078 CTGACCCGGAGAGAGCCCTTACCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1137

Db 1461 CTGACCCGGAGAGAGAGCTTACCTTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1520

Qy 1138 TGTGTGTTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1197

Db 1521 TGTGTGTTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1580

Qy 1198 GTGCCCCCATGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1257

Db 1581 GTACCCGATGGCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1640

Qy 1258 CTTGTATCTACACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1317

Db 1641 CTTGTATCTACACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1700

Qy 1318 CGCCCGTGACCCAGACGCGCTGTGTA 1344

Db 1701 CGCCCGTGACCCAGACGCGCTGTGTA 1727

RESULT 15

AC112830 276543 bp DNA linear HTG 21-SEP-2002

LOCUS Rattus norvegicus clone CH230-46115, *** SEQUENCING IN PROGRESS

DEFINITION *** 2 unordered pieces.

ACCESSION AC112830 GI:23266028

VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 276543)

1. Muzny, D., Marzke, M., Lee, S., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooke, S., Amin, A., Angulano, D., Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabriel, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregergs, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Huylk, S., Hume, J., Idelbird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyvet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowls, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenz, L., Louie, L., Louie, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhood, S., McLeod, M.P., McNeill, T.Z., Meenan, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankwelu, O., Okunolu, G., Olarnpunsoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poldinger, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,

Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Saverly, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sherry, D., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smaj, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sos, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 276543)

Worley, K.C.

Direct Submission

Submitted (25-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 276543)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 21, 2002 this sequence version replaced gi:21742229.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rac/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GRPQ

Center clone name: CH230-46115

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 237012 bases at least Q40

Consensus quality: 239346 bases at least Q30

Consensus quality: 240985 bases at least Q20

Estimated insert size: 252028; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

1 275384 contig of 275384 bp in length

275385 275484 gap of unknown length

275485 276543 contig of 1059 bp in length.

Location/Qualifiers

1. 276543

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-46115"

1. 1265

/note="wgs_end_extension"

misc_feature

FEATURES

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clone_end:Sp6"
misc_feature      274215..275384
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clone_end:Sp6"

BASE COUNT      60488 a 57855 c 60622 g 63094 t 34444 others
ORIGIN
Query Match      74.2%; Score 996.8; DB 2; Length 276543;
Best Local Similarity 84.7%; Pired. No. 6.2e-158;
Matches 1142; Conservative 0; Mismatches 202; Indels 4; Gaps 2;

QY      1      ATGAGACCAAGAGACCCCTTCTCCGTCAGAGCCAGCCGCGCATPAGCGGGCGCATACC 60
DB      109542  ATGAGACCATAGAGACCCCTTCTCCGTCAGAGCCAGCCGCGCATPAGCGGGCGCATACC 109601
QY      61      TTCTCATCTCTTTACCATCTTCGAGCAGCTCTGATCTCTGAGCTGTGTGACAGC 120
DB      109602  TTCTCATCTCTTTACCATCTTTGCGCAATGCGGTGTCATCTGCTGTGTGACAGC 109661
QY      121     CGCTCGTGGCGCCCTCTAGAACTGTCTCTGCTGCTGCGCCCGCGCATCTG 180
DB      109662  CGCTCATCTGTCAGCAAAACCTGTCTCTGCTGTCATGCGCAGCGCATCTCTA 109721
QY      181     GTGGCCACGCTCATCTCTCTTTCTGCTGCGCCAGCAGAGCTGTGGGCTTCTGTATTC 240
DB      109722  GTGGCTACTCTCATCTCTCTCTCTCTCTGCGCCAGCAGAGCTGTGGGCTTCTGTATTC 109781
QY      241     CGGCGCAGCTGTGGTCAGAGTGTACTCTGCGCTGACGTCCTCTGCACTCTGTCATC 300
DB      109782  TGGGTCGCTGTGTGTCAGAGTGTACTCTGCGCTGACGTCCTCTCTGTCATCTCTCATC 109841
QY      301     GTGCACTGTGCGGCATCAAGCTGAGCGCTACTGAGCGCGTGAAGCGCGCGCTGAGTAC 360
DB      109842  GTGCACTGTGTGTCATCAAGCTGAGCGCTACTGAGCGCGTGAAGCGCGCATTTGAGTAC 109901
QY      361     AACTCCAGAGGACCCCGCGCGCATCAAGTGTACTCTCTCACTGTGTGGCTCATGCC 420
DB      109902  AACTCCAGAGGACCTCCGCGCGCATCAAGTGTACTCTCTCACTGTGTGGCTCATTTGCA 109961
QY      421     GCGGTACTGTGCGCGCGCGCGCTCATCTAACAAGGGGCGACAGGGCGCGCGCGG 480
DB      109962  GCTGTCACTTGTCTAAGCGCGCGCTCATCTAACAAGGGGCGACAGCGCGCGCGG 110021
QY      481     CGCCCCAGTGCAGACTCAACAGAGAGCGCTGTACTCTGCTGCTCCAGCATGATCT 540
DB      110022  CTCCCGCAGTGTAGCTCAACAGAGAGCGCTGTACTCTGCTGCTCCAGCATGATCT 110081
QY      541     TTCTTGTCTCTGCTCTCATCATGATCTTGTCTTACTCTGCGCATCTAAGTATGCCAAA 600
DB      110082  TTTTGTCTCTGCTCTCATCATGATCTCTGTCTAAGTATCTAAGTATGCCAAA 110141
QY      601     CGAGGCAACCGCAAGGTCCCAAGGGGCGAGGGGCGCTGGCGAGGGTGAAGTCAAGCAG 660
DB      110142  CGAGGCAACCGCAAGGTCTCGAGGCCAAGGGGCGCTGTGAGAGAGGTGATCAAGAGAG 110201
QY      661     CCCCAGCCCGACATGTGTGGGCTTTGGCTCAGCCAACTGCGAGCGCTGGGCT---CT 717
DB      110202  CCCCAGCCCGGTGTGTGGGGAGGTGCAACTCAGCTAAGGTGCCACCGCTGTCTCTCT 110261
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QY      718     GTGGCTTGTCCAGAGAGGTCAACGACACTCGAAGTCCACTGGGGAGAGAGAGGGG 777
DB      110262  CTATCTTGTGTGAGAGGCGCAATGAGCACCCCAAGCTCTCAAGAGAGAGAGAGGGG 110321
QY      778     GAGACCCCTGAAAGATCTGAGACCCGGGCTTGGCCACCAGTTGGGCTCCCTCCCAAC 837
DB      110322  GAGACCCCTGAAAGATCTTGAAGCCAGGGCTTGGCCCAACTGGTGTCTCCCTCCCAAG 110381
QY      838     TCAGGCCAGAGGCGAAGAGAGGGGTGTGTGTGGGGCATCTCAAGAGATGAAGTGAAG 897
DB      110382  TCAGGCCAGAGGCGAAGAGAGGGGACTTATGTGGGGCATCTCAAGAGAGAGAGATGAAG 110441
QY      898     GAGAGAGAGAGAGAGAGAGTGTGAACCCAGGAGTCCAGTGTCTCCGCGCTCAGCT 957
DB      110442  GATGAGAGAGAGTGTGAAGATGTGAACCCAAACCTGCGAGCATCTCGCTCGGTGA 110501
QY      958     TGCAGCCCGCGCTGTCAGAGCCAGGAGCTCCCGGCTGTGGCCACCTTACGTGGCCAG 1017
DB      110502  TGCAGCCCAACCTTGCAGAGGCTCAGACTCTCGGGTACTGGCCACACTTCTGTGGCCAG 110561
QY      1018    GTGCTCTGTGGCAGAGGCGTGGGTGCTATAGGTGGCAGTGGTGGGTGGAAGGGCGCAG 1077
DB      110562  GTGCTTCTGTGGCAGAGATGTGGAGTTGCCAAGTGGCAGTGTGGCGCAGAGCGACAG 110621
QY      1078    CTGACCCGGGAGAGAGCGCTTCACTTCTGTGCTGCTGTGTGCTATTGGCGTTTGTGCTC 1137
DB      110622  CTGAGCGGGAGAGAGAGGTTTCACTTGTGTGCTGCTGTGTGCTATTGGAGTTTGTGTGCTC 110681
QY      1138    TGTGTGTTCCCTCTTCTTTCAGCTACAG-CTGGGCGCATCTGCCCCAGACCTGCA 1196
DB      110682  TGTGTGTTCTTCTTCTTTCAGCTACAGCCCTGGGGGCGCATCTGCCCCAGACCTGCA 110741
QY      1197    GGTGCCCATAGGCTCTTCCAGTTCTTCTTGTGATGAGTACTGCAACAGCTCACTGA 1256
DB      110742  GGTACCGCATGGCTCTTCCAGTTCTTCTTGTGATGAGTACTGCAACAGCTCTTGA 110801
QY      1257    CCTGTATCTACACCATCTTCAACAGAGACTTCCGCGGTGCTTCGAGAGATCTGTG 1316
DB      110802  CCTGTATCTACACCGTCTTCAACAGAGACTTCCGCGGTGCTTCGAGAGATCTGTG 110861
QY      1317    CCGCCCGTGAAGCCAGACGCGCTGTGA 1344
DB      110862  CCGCCCGTGAAGCCAGACTGTGTGA 110889
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Search completed: February 7, 2004, 23:41:25
Job time : 5093.97 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:41:41 ; Search time 393.682 Seconds
(without alignments)
9215.676 Million cell updates/sec

Title: US-09-692-077d-2

Perfect score: 1344
Sequence: 1 atgaccaccagagaccctca.....ggaccacagcgccgtgta 1344

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues.

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 4: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA1983.DAT:*
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- 23: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT:*
- 25: /SIDSI/gcgdata/geneSeq/geneSeqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|------------------------------|
| 1 | 1344 | 100.0 | 1344 | 23 | AA199906 Human alpha-2B-AR t |
| 2 | 1339.2 | 99.6 | 1344 | 22 | AA004761 Human alpha-2B-AR t |
| 3 | 1339.2 | 99.6 | 1344 | 24 | AA044388 Human alpha-2B-AR t |
| 4 | 1325 | 98.6 | 1353 | 23 | AA199905 Human alpha-2B-AR t |
| 5 | 1323.4 | 98.5 | 1353 | 22 | AA004762 Human alpha-2B-AR t |
| 6 | 1323.4 | 98.5 | 1353 | 24 | AA044389 Human alpha-2B-AR t |
| 7 | 1321.8 | 98.3 | 2072 | 25 | ACAS6583 Human alpha-2B-AR t |
| 8 | 1321.8 | 98.3 | 3274 | 25 | ABZ42624 Human alpha-2B-AR t |

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|------------------------------|
| 9 | 1302.6 | 96.9 | 2064 | 12 | AA014151 Human alpha 2 beta |
| 10 | 1302.6 | 96.9 | 2064 | 18 | AA199906 Human alpha-2B-AR t |
| 11 | 617.6 | 46.0 | 6904 | 24 | AB132075 Human immune syste |
| 12 | 617.6 | 46.0 | 6904 | 24 | AB28365 Human chemically t |
| 13 | 531.6 | 39.6 | 6904 | 24 | AB132074 Human immune syste |
| 14 | 531.6 | 39.6 | 6904 | 24 | AB28364 Human chemically t |
| 15 | 459.4 | 34.2 | 1383 | 23 | AA199931 Human alpha-2C-AR e |
| 16 | 457.8 | 34.1 | 2826 | 25 | AB246625 Human alpha-2C-AR t |
| 17 | 446 | 33.2 | 1350 | 23 | AA199918 Human alpha-2A-AR v |
| 18 | 445.4 | 33.1 | 3653 | 25 | AB242623 Human alpha-2A-AR v |
| 19 | 445 | 33.1 | 1382 | 15 | AA064890 Human derived adre |
| 20 | 445 | 33.1 | 1382 | 24 | AB235643 Human gene express |
| 21 | 445 | 33.1 | 1382 | 25 | ACB56658 Human signaling p |
| 22 | 444.6 | 33.1 | 1371 | 23 | AA199933 Human alpha-2C-AR v |
| 23 | 444.4 | 33.1 | 1350 | 23 | AA199917 Human alpha-2A-AR v |
| 24 | 432.6 | 32.2 | 3604 | 25 | ACB56582 Human signaling p |
| 25 | 304.2 | 22.6 | 1758 | 24 | AB235339 Human gene express |
| 26 | 269.8 | 20.1 | 4850 | 24 | AB28395 Human chemically t |
| 27 | 262.6 | 19.5 | 1733 | 24 | AB047500 Oligonucleotide fo |
| 28 | 262.6 | 19.5 | 1733 | 24 | AB047501 Oligonucleotide fo |
| 29 | 262.6 | 19.5 | 7353 | 24 | AB132073 Human immune syste |
| 30 | 262.6 | 19.5 | 7353 | 24 | AB28363 Human chemically t |
| 31 | 210.4 | 15.7 | 1140 | 18 | AA188392 Corn barnacle G-pr |
| 32 | 184.8 | 13.8 | 3125 | 23 | AB113003 Drosophila melanog |
| 33 | 184.8 | 13.8 | 3335 | 13 | AA021928 Drosophila melanog |
| 34 | 183.2 | 13.6 | 6313 | 23 | AB113002 Oligonucleotide fo |
| 35 | 181.4 | 13.5 | 1733 | 24 | AB047498 Oligonucleotide fo |
| 36 | 181.4 | 13.5 | 1733 | 24 | AB047499 Oligonucleotide fo |
| 37 | 181.4 | 13.5 | 7353 | 24 | AB132072 Human immune syste |
| 38 | 181.4 | 13.5 | 7353 | 24 | AB28362 Human chemically t |
| 39 | 171 | 12.7 | 1431 | 18 | AA188394 Human amphitrite |
| 40 | 165.8 | 12.3 | 4850 | 24 | AA188395 Human chemically t |
| 41 | 158.6 | 11.8 | 921 | 15 | AA072324 Partial human alph |
| 42 | 158.6 | 11.8 | 921 | 16 | AA11608 Human alpha-1B adr |
| 43 | 158.6 | 11.8 | 1567 | 15 | AA087879 Human/rat alpha-1B |
| 44 | 158.6 | 11.8 | 1567 | 16 | AA11615 Human/rat hybrid a |
| 45 | 158.6 | 11.8 | 1738 | 15 | AA062817 Genomic sequence e |

ALIGNMENTS

RESULT 1
AA199906
ID AA199906 standard; DNA; 1344 BP.
AC AA199906;
XX
DT 18-FEB-2002 (first entry)
DE Human alpha-2B-AR third intracellular loop variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2B-AR; chromosome 2; ds.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FH 1..1344
FT CDS
FT /tag= a
FT /product= "alpha-2B-AR"
FT /note= "sequence is deleted for a 9 nucleotide
polymorphic site found at nucleotides 901-909
of the wildtype alpha-2B-AR protein (AA199905)"
PN WO200179561-A2.
PD 25-OCT-2001.
XX
XX 17-APR-2001; 2001WO-US12575.
XX

PR 17-APR-2000; 2000US-0551744.
PR 10-AUG-2000; 2000US-0636259.
PR 19-OCT-2000; 2000US-0692077.
XX (LIGS/) LIGSETT S B.
PA (SMAL/) SMALL K M.
XX LIGSETT SB, Small KM;
XX WPI: 2001-611728/70.
DR P-PSDB; NAM52118.
XX
XX Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting
PT a polymorphic site -
XX
XX Claim 5; Page 144-145; 163p; English.

CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising;
CC (a) obtaining a sample having a polynucleotide encoding an alpha-2B,
CC alpha2A or alpha2C, or fragment or complement of; and
CC (b) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (IIIV)
CC or a site comprising (A) (999GCG99GCG) or (B) (999GCG99GCG) at
CC positions 961-972 of (III). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2B, alpha2A, or alpha2C agonist (e.g. ephedrine,
CC norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, ARC 239,
CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to the ability to
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide
CC polymorphic site found at nucleotides 901-909 of the wildtype gene
CC (AAI99905).
XX
XX

SO Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 other;

Query Match 100.0%; Score 1344; DB 23; Length 1344;
Best Local Similarity 100.0%; Pred. No. 8.6e-259;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGACACAGAGACCCCTACTCCGTGAGGCAAGGCGCATAGGCGGCGCATAC 60
DB 1 ATGAGACACAGAGACCCCTACTCCGTGAGGCAAGGCGCATAGGCGGCGCATAC 60
QY 61 TTCTCATCTCTTACCATCTTGGGCAAGGCTCTGTCATCTGTCGTGTTGACGAG 120
DB 61 TTCTCATCTCTTACCATCTTGGGCAAGGCTCTGTCATCTGTCGTGTTGACGAG 120
QY 121 CGCTCGTGGCGGCCCTCAGAACCTGTTCTGTCGTGTCGCGCGCGGACATCTTG 180
DB 121 CGCTCGTGGCGGCCCTCAGAACCTGTTCTGTCGTGTCGCGCGCGGACATCTTG 180
QY 181 GTGGCAAGGCTCATCATCCCTTCTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCG 240
DB 181 GTGGCAAGGCTCATCATCCCTTCTGTCGTGTCGTCGTCGTCGTCGTCGTCGTCG 240
QY 241 CGGCGCAAGTGTGTGAGGTGTACCTGCGCTGACGTCGTCGTCGTCGTCGTCGTC 300
DB 241 CGGCGCAAGTGTGTGAGGTGTACCTGCGCTGACGTCGTCGTCGTCGTCGTCGTC 300
QY 301 GTGCACTGTGCGCATCAGCTGAGCCGCTGAGCCGTCGTCGTCGTCGTCGTCGTC 360
DB 301 GTGCACTGTGCGCATCAGCTGAGCCGCTGAGCCGTCGTCGTCGTCGTCGTCGTC 360

DB 301 GTGCACTGTGCGCATCAGCTGAGCCGCTGAGCCGTCGTCGTCGTCGTCGTCGTC 360
QY 361 AACTCCAGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
DB 361 AACTCCAGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 421 GCGTCATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480
DB 421 GCGTCATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480
QY 481 CGCCCAAGTGTGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 540
DB 481 CGCCCAAGTGTGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 540
QY 541 TTCTTGTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 600
DB 541 TTCTTGTCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 600
QY 601 CGCAGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
DB 601 CGCAGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 CCCGACCGGACGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 720
DB 661 CCCGACCGGACGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 720
QY 721 GCTTCTGCAAGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 780
DB 721 GCTTCTGCAAGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 780
QY 781 ACCCTGAAGATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 840
DB 781 ACCCTGAAGATCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 840
QY 841 GGCAGAGGCGGCAAGAGGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 900
DB 841 GGCAGAGGCGGCAAGAGGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 900
QY 901 GAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
DB 901 GAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
QY 961 AGCCCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
DB 961 AGCCCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020
QY 1021 CTCTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1021 CTCTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
QY 1081 ACCCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1081 ACCCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 TGGTTCCTCTCTTCTTCAAGCTACAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1200
DB 1141 TGGTTCCTCTCTTCTTCAAGCTACAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1200
QY 1201 CCCGATGAGGCTCTTCAAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1260
DB 1201 CCCGATGAGGCTCTTCAAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1260
QY 1261 GTTATCTACACCATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
DB 1261 GTTATCTACACCATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
QY 1321 CGGTGAGCCAGAGCGGCTGTGTA 1344
DB 1321 CGGTGAGCCAGAGCGGCTGTGTA 1344

RESULT 2
AAD04761

DB 1141 TGGTCCCTTCTTCTTACGATACAGCTGGGGGCGCATCTGCCGAGACATGCAAGTG 1200
QY 1201 CCCATGAGCTCTTCCAGATTCTTCTTGTGATCGGCTACTGCAACAGCTCACTGAACCT 1260
DB 1201 CCCATGAGCTCTTCCAGATTCTTCTTGTGATCGGCTACTGCAACAGCTCACTGAACCT 1260
QY 1261 GTTATCTACACATCTTCAACAGAGACTCCGCGGCTTCCGAGAGATCCTGAGCCG 1320
DB 1261 GTTATCTACACATCTTCAACAGAGACTCCGCGGCTTCCGAGAGATCCTGAGCCG 1320
QY 1321 CCGTGAACCCAGACGCGCTGTGA 1344
DB 1321 CCGTGAACCCAGACGCGCTGTGA 1344
RESULT 3
AAD44388
ID AAD44388 standard; DNA; 1344 BP.
AC AAD44388;
AT 13-DEC-2002 (first entry)
DE Human alpha-2B-adrenoceptor variant DNA.
XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KW hypertension; hypotensive; variant; gene; de.
OS Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT CDS 1..1344
FT /*tag= a
FT /product= "Human alpha-2B-adrenoceptor variant
FT protein"
XX WO20026617-A1.
XX 29-AUG-2002.
XX 13-FEB-2002; 2002MO-FI00113.
XX 20-FEB-2001; 2001FI-0000323.
XX (JURI-) JURILAB LTD OY.
XX Salonen J;
XX WPI; 2002-667063/71.
XX P-PSDB; ABE26633.
XX Detecting a risk of hypertension and targeting treatment in a subject
XX by determining the pattern of alleles encoding a variant
XX alpha-2-adrenoceptor -
XX PS Disclosure; Page 24-26; 35bp; English.
XX The invention relates to a method for detecting a risk of hypertension
XX by determining the pattern of alleles encoding a variant alpha-2B-
XX adrenoceptor (AR) protein. The methods and compositions of the invention
XX are useful for detecting risks and targeting treatment for hypertension.
XX The kit is also useful for selecting for clinical drug trials testing
XX the antihypertensive effect of compounds. The present sequence is human
XX alpha-2B-adrenoceptor variant DNA.
SQ Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 other;
Query Match 99.6%; Score 1339.2; DB 24; Length 1344;
Best Local Similarity 99.8%; Pred. No. 7.8e-258;
Matches 1341; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAGACCAAGAGACCCCTACTCCGTGACAGGCCACAGCGGCATTAGCGGCGCATCACC 60

DB 1 ATGAGACCAAGAGACCCCTACTCCGTGACAGGCCACAGCGGCATTAGCGGCGCATCACC 60
QY 61 TTCTCATTTCTTTTACATCTTCCGCAACGCTCTGTGATCTCTGCTGTGTGACACG 120
DB 61 TTCTCATTTCTTTTACATCTTCCGCAACGCTCTGTGATCTCTGCTGTGTGACACG 120
QY 121 CGCTGCTGCGCCCTCAGAACCTGTTCTGTGCTGAGCCGCGCCGCAATCTG 180
DB 121 CGCTGCTGCGCCCTCAGAACCTGTTCTGTGCTGAGCCGCGCCGCAATCTG 180
QY 181 GTGGCCACGCTATCATCTCTTTCTGTGCTGAGCCGCGCCGCAATCTG 240
DB 181 GTGGCCACGCTATCATCTCTTTCTGTGCTGAGCCGCGCCGCAATCTG 240
QY 241 CGGCGACAGTGTGACAGGTGATCTGAGGCTGACGATGCTCTTCTGCACTGTGATC 300
DB 241 CGGCGACAGTGTGACAGGTGATCTGAGGCTGACGATGCTCTTCTGCACTGTGATC 300
QY 301 GTGCACTGTGCGCATACGCTGAGCGGCTACTGAGCCGCTGAGCGCGTGGAGTAC 360
DB 301 GTGCACTGTGCGCATACGCTGAGCGGCTACTGAGCCGCTGAGCGCGTGGAGTAC 360
QY 361 AACTCAAGGAGACCCCGCGCATCAAGTGCATCATCTGATCTGTGCTCATCGCC 420
DB 361 AACTCAAGGAGACCCCGCGCATCAAGTGCATCATCTGATCTGTGCTCATCGCC 420
QY 421 GCGGTATCTGCTGCGCCCTCTCATCAAGAGCGACAGAGCCCGCAGCGCGG 480
DB 421 GCGGTATCTGCTGCGCCCTCTCATCAAGAGCGACAGAGCCCGCAGCGCGG 480
QY 481 CGGCGCATGGAAGTCAACAGAGAGCTGTGATCTGTGCTCTGAGCTCAAGCT 540
DB 481 CGGCGCATGGAAGTCAACAGAGAGCTGTGATCTGTGCTCTGAGCTCAAGCT 540
QY 541 TTCTTGTCTTGTGCTCATCATGATCTGTGCTGCTGAGCTCAAGCTCAAGCT 600
DB 541 TTCTTGTCTTGTGCTCATCATGATCTGTGCTGCTGAGCTCAAGCTCAAGCT 600
QY 601 CGGAGCAACCGAGAGTCCAGAGGCGCAAGAGAGAGAGAGAGAGAGAG 660
DB 601 CGGAGCAACCGAGAGTCCAGAGGCGCAAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 CCCGACCGACATGATGAGGCTTTGAGCTCAAGCAACTGAGCCCTGCTGTG 720
DB 661 CCCGACCGACATGATGAGGCTTTGAGCTCAAGCAACTGAGCCCTGCTGTG 720
QY 721 GCTTGTGCAAGAGTCAAGCACTGCAAGTCACTGAGAGAGAGAGAGAGAG 780
DB 721 GCTTGTGCAAGAGTCAAGCACTGCAAGTCACTGAGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTGAAGTACTGAGACCCGAGCTTGTGCAAGTCACTGAGAGAGAGAGAG 840
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QY 841 GAGCAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GAGCAGAGCAG 900
QY 901 GAG 960
DB 901 GAG 960
QY 961 AGCGCCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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QY 1021 CTCTGTGAG 1080
DB 1021 CTCTGTGAG 1080
QY 1081 ACCCGAG 1140

| DB | Accession | Gene | Chromosome | Position | Strand | Length | GC Content | Repeat | SNP | Indel | Other |
|----|-----------|--|------------|----------|--------|--------|------------|--------|-----|-------|-------|
| Db | 1081 | ACCCGGAGAACGCGCTTACCTTCGTCGTCGGCTGTCGTCATTTGGCGTTTGTGCTC | 11 | | | | | | | | |
| Qy | 1141 | TGTTTCCCTTCTTCTTCAAGCTACAGCTTGGGCGCATCTGCCCGAAGACTGCAAGTG | 120 | | | | | | | | |
| Db | 1141 | TGGTTTCCCTTCTTCTTCAAGCTACAGCTTGGGCGCATCTGCCCGAAGACTGCAAGTG | 120 | | | | | | | | |
| Qy | 1201 | CCCGATGGCGCTTCTTCAGTTCTTCTTCTTGGATCGGCTATGCAAGCTCAGTGAACCT | 126 | | | | | | | | |
| Db | 1201 | CCCGATGGCGCTTCTTCAGTTCTTCTTCTTGGATCGGCTATGCAAGCTCAGTGAACCT | 126 | | | | | | | | |
| Qy | 1261 | GTTATCTACACCATCTTCAACGAGACTTCGCGCGCTTCGAGAGATCTGTGCCG | 132 | | | | | | | | |
| Db | 1261 | GTTATCTACACCATCTTCAACGAGACTTCGCGCGCTTCGAGAGATCTGTGCCG | 132 | | | | | | | | |
| Qy | 1321 | CCGTGAGCCGACGAGCGGCTGTGGA 1344 | | | | | | | | | |
| Db | 1321 | CCGTGAGCCGACGAGCGGCTGTGGA 1344 | | | | | | | | | |

RESULT 4
AA199905
ID AA199905 standard; DNA; 1353 BP.
AA199905;
18-FEB-2002 (first entry)
Human alpha-2BAR third intracellular loop encoding DNA.
Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; GenBank Accession AF009500; chromosome 2; de.
Homo sapiens.
Key Location/Qualifiers
CDS 1..1353
/*tag= a
/product= "alpha-2BAR"
/note= "sequence includes a 9 nucleotide polymorphic site at nucleotides 901-909 absent in the alpha-2BAR variant. (AA199906)"
XN WC200179561-A2.
XN 25-OCT-2001.
XN 17-APR-2001; 2001WO-US12575.
XN 17-APR-2001; 2000US-0551744.
XN 10-AUG-2000; 2000US-0636259.
XN 19-OCT-2000; 2000US-0692077.
XN (LIGG/) LIGGETT S B.
XN (SMAL/) SMALL K M.
XN LIGgett SB, Small KM;
XN WPI; 2001-611728/70.
XN P-PSDB; AAM52117.
XN Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting a polymorphic site -
XN Claim 4; Page 144; 163p; English.
XN The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising;
XN (a) obtaining a sample having a polynucleotide encoding an alpha-2B,

CC alpha2A, alpha2C or fragment or complement of; and
CC (D) detecting a polymorphic site comprising nucleotide positions 901-909
CC of (I), a site comprising cytosine or guanine at position 753 of (11V)
CC or a site comprising (A) (999c999gcgcg) or (B) (999gcgcgcga) at
CC positions 961-972 of (111). The method may be used for genotyping an
CC alpha2B, alpha2A or alpha2C receptor gene and further used to determine
CC whether an individual is at increased risk of developing a disease
CC associated with alpha2B, alpha2A or alpha2, comprising detecting a
CC polymorphic site which correlate to disease selected from cardiovascular
CC disease, central nervous system disease and combinations of these. In
CC addition, the technique may be used to predict an individual's response
CC to an alpha2A, alpha2A, or alpha2C agonist (e.g. epinephrine,
CC norepinephrine, clonidine, oxymetazoline (e.g. guanabenz, UK14304, BHT933 and
CC combinations of these) or antagonist (e.g. yohimbine, prazosin, AHC 239,
CC rauwolfine, idazoxan, tolazoline, phenolamine and combinations of
CC these) by detecting the polymorphic site and correlating the site to a
CC predetermined response (where the response is correlated to adenylyl
CC cyclase, MAP kinase activity, phosphorylation or inositol phosphate
CC levels). The present sequence is that of the third intracellular loop of
CC the human alpha-2BAR (Genbank Accession AF009500), the sequence includes
CC a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the
CC alpha-2BAR variant (AA199906).
XX
XQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 other;

| | | | | |
|-----------------------|--------|-------------------|-------|-------------|
| Query Match | 98.64% | Proc. No. 1325 | DB 23 | Length 1353 |
| Best Local Similarity | 99.34% | Proc. No. 5.3e-25 | | |
| Matches 1344 | 0 | Mismatches | 0 | Indels 9 |
| | | | | Gaps 1 |

[illegible]

QY 661 CCCGACCCGACCACTGCTGAGGCTTTGAGCTCAAGCCAAATGCGAGCCCTGAGCTCTGTG 720
 Db 661 CCCGACCCGACCACTGCTGAGGCTTTGAGCTCAAGCCAAATGCGAGCCCTGAGCTCTGTG 720
 QY 721 GCTTCTGCGAGAGAGTCAACGACACTCGAAGTCACTGAGGAGAAAGAGAGAGAGAGAG 780
 Db 721 GCTTCTGCGAGAGAGTCAACGACACTCGAAGTCACTGAGGAGAAAGAGAGAGAGAGAG 780
 QY 781 ACCCTGAGAGATCTGAGGAGCCCGGCTTTCACACCCAGTTGGGCTGCGCTTCCCACTCA 840
 Db 781 ACCCTGAGAGATCTGAGGAGCCCGGCTTTCACACCCAGTTGGGCTGCGCTTCCCACTCA 840
 QY 841 GCGCAGGAGCAG 894
 Db 841 GCGCAGGAGCAG 894
 QY 895 ---GAG 951
 Db 901 GAAAG 960
 QY 952 TCAGCTTGCAGAGCCCGCTGAG 1011
 Db 961 TCAGCTTGCAGAGCCCGCTGAG 1020
 QY 1012 GCGCAGAGTCTCTCTGAG 1071
 Db 1021 GCGCAGAGTCTCTCTGAG 1080
 QY 1072 GCGCAGAGTCTCTCTGAG 1131
 Db 1081 GCGCAGAGTCTCTCTGAG 1140
 QY 1132 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
 Db 1141 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 QY 1192 TGCAAGGTGCGCCAG 1251
 Db 1201 TGCAAGGTGCGCCAG 1260
 QY 1252 CTGAACCTGTTATCTTACATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1311
 Db 1261 CTGAACCTGTTATCTTACATCTTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 QY 1312 CTGTCGCGCCCGTGAAG 1344
 Db 1321 CTGTCGCGCCCGTGAAG 1353
 RESULT 5
 AAD04762 ID AAD04762 standard; DNA; 1353 BP.
 XX AAD04762;
 AC
 XX 04-JUL-2001 (first entry)
 DT
 XX Human alpha2B-adrenoceptor (alpha2B-AR) gene.
 DE
 XX Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
 KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
 KW norepinephrine; epinephrine; therapy; vascular contraction;
 KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
 KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..1353
 FT /tag= a
 FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
 protein"
 XX

PN WC0200129082-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 20-OCT-2000; 2000MO-F100913.
 XX
 PR 22-OCT-1999; 99US-0422985.
 XX
 PA (JUVA-) JUVANTIA PHARMA LTD OY.
 XX
 PI Snipir A, Heinoonen P, Alhopuro P, Karonen M, Koulu M, Pesonen U;
 PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyysioenen K;
 PI Salonen R, Kaunonen J, Valkonen V,
 XX
 DR WPI; 2001-300318/31.
 DR P-PSDB; AAB00990.
 XX
 PT New DNA molecule encoding variant specific adrenoceptor protein with
 PT deletion of specific amino acids located in the third intracellular
 PT loop of the polypeptide, for treating vascular contraction of coronary
 PT arteries -
 XX
 PS Disclosure; Page 27-29; 37pp; English.
 XX
 CC The present sequence is a gene encoding human alpha2B-adrenoceptor
 CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
 CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
 CC acids (amino acids 294-311), located in the third intracellular loop of
 CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
 CC Alpha2-AR mediate many of the physiological effects of the
 CC catecholamines, norepinephrine and epinephrine. An antagonist of
 CC alpha2B-adrenoceptor is useful for treating a mammal suffering from
 CC vascular contraction of coronary arteries and a disease involving
 CC as coronary heart disease (CHD), unstable chronic angina pectoris which is
 CC clinically expressed as Prinzmetal's variant form or acute myocardial
 CC infarction (AMI). Alpha2B-AR gene is used in gene therapy.
 XX
 SO Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
 Query Match 98.5%; Score 1323.4; DB 22; Length 1353;
 Best Local Similarity 99.3%; Pred. No. 1.1e-254;
 Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;
 QY 1 ATGGAACACAG 60
 Db 1 ATGGAACACAG 60
 QY 61 TTCCTCATCTCTTACATCTTACATCTTACATCTTACATCTTACATCTTACATCTTACATCT 120
 Db 61 TTCCTCATCTCTTACATCTTACATCTTACATCTTACATCTTACATCTTACATCTTACATCT 120
 QY 121 CGCTGCTGCGCGCCCTGAG 180
 Db 121 CGCTGCTGCGCGCCCTGAG 180
 QY 181 GTGGCAGAGCTCATATCCCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 Db 181 GTGGCAGAGCTCATATCCCTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 241 CGGCGAGAGTGTGAG 300
 Db 241 CGGCGAGAGTGTGAG 300
 QY 301 GTGCACTGTGAG 360
 Db 301 GTGCACTGTGAG 360
 QY 361 AACTCAAG 420
 Db 361 AACTCAAG 420
 QY 421 GCGCTCATCTGCTGCGCGCCCTGATCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

Db 421 GCGCTACTCTGCTGCGCGCCCTCATCTACAGGCGCCAGCGGCCCGCCGCGGG 480
QY 481 CGCCCCAGTGCAGAGCTCAACACAGAGAGCGCTGTATACCTCGGCTCAGCATGATCT 540
Db 481 CGCCCCAGTGCAGAGCTCAACACAGAGAGCGCTGTATACCTCGGCTCAGCATGATCT 540
QY 541 TTCTTGTCTCTTGTCTCATCATGATCTTGTCTACCTGGCATCTACCTGATGCCAA 600
Db 541 TTCTTGTCTCTTGTCTCATCATGATCTTGTCTACCTGGCATCTACCTGATGCCAA 600
QY 601 CGCAGCAACCGCAGAGGTCCAGAGGCCAAGGGGGGGCTGGGCAAGGTGATCCAGCAG 660
Db 601 CGCAGCAACCGCAGAGGTCCAGAGGCCAAGGGGGGGCTGGGCAAGGTGATCCAGCAG 660
QY 661 CCCGACCCGACATGCTGGGGGCTTTGGCCCTACAGCCAACTGCCAGCCCTGGCTCTGTG 720
Db 661 CCCGACCCGACATGCTGGGGGCTTTGGCCCTACAGCCAACTGCCAGCCCTGGCTCTGTG 720
QY 721 GCTTCTGCGAGAGAGGTCAACCGACACTCGAAGTCTACTGGGAGAGAGAGAGAGAG 780
Db 721 GCTTCTGCGAGAGAGGTCAACCGACACTCGAAGTCTACTGGGAGAGAGAGAGAGAG 780
QY 781 ACCCTGGAATATCTGGGACCCCGGGCTTGTGCACCCAGTTGGGCTGCTTCCCACTCA 840
Db 781 ACCCTGGAATATCTGGGACCCCGGGCTTGTGCACCCAGTTGGGCTGCTTCCCACTCA 840
QY 841 GGGCAGGGCCAGAGAGAGGGGTTGTGGGGCATCTCCAGATGAGTGAAGTGA----- 894
Db 841 GGGCAGGGCCAGAGAGAGGGGTTGTGGGGCATCTCCAGATGAGTGAAGTGAAGAGAG 900
QY 895 ---GAG 951
Db 901 GAAAG 960
QY 952 TCAGCTTTCAG 1011
Db 961 TCAGCTTTCAG 1020
QY 1012 GGGCAGAGTGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1071
Db 1021 GGGCAGAGTGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1072 GGGCAGAGTGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1131
Db 1081 GGGCAGAGTGTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1132 GTGCTGTGCTGTCT 1191
Db 1141 GTGCTGTGCTGTCT 1200
QY 1192 TGCAGAGTGTCT 1251
Db 1201 TGCAGAGTGTCT 1260
QY 1252 CTGACCTGTGTCT 1311
Db 1261 CTGACCTGTGTCT 1320
QY 1312 CTGTGCGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1344
Db 1321 CTGTGCGCGCGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1353

RESULT 6
AAD4389
XX AAD4389 standard; DNA; 1353 BP.
XX AAD4389;

DT 13-DEC-2002 (first entry)
XX
DE Human alpha-2B-adrenoceptor gene.

XX
KM Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KM hypertension; hypotensive; gene; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1353
FT /*tag= a
FT /product= "Human alpha-2B-adrenoceptor protein"
XX
PN W020026617-A1.
XX
PD 29-AUG-2002.
XX
PF 13-FEB-2002; 2002MO-F100113.
XX
PR 20-FEB-2001; 2001FI-0000323.
XX
PA (JURI-) JURILAB LTD OY.
XX
PI Salonen J.
XX
DR WPI; 2002-667063/71.
DR P-PSDB; AAE26634.
XX
PT Detecting a risk of hypertension and targeting treatment in a subject
PT by determining the pattern of alleles encoding a variant
PT alpha-2-adrenoceptor
XX
PS Disclosure; Page 27-29; 35pp; English.
XX
CC The invention relates to a method for detecting a risk of hypertension
CC by determining the pattern of alleles encoding a variant alpha-2B-
CC adrenoceptor (AR) protein. The methods and compositions of the invention
CC are useful for detecting risks and targeting treatment for hypertension.
CC The kit is also useful for selecting for clinical drug trials testing
CC the antihypertensive effect of compounds. The present sequence is human
CC alpha-2B-adrenoceptor gene.
XX
SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 other;
Query Match 98.5%; Score 1323.4; DB 24; Length 1353;
Best Local Similarity 99.3%; Pred. No. 1.1e-254;
Matches 1343; Conservative 0; Mismatches 1; Indels 9; Gaps 1;
QY 1 ATGAGACACAG 60
Db 1 ATGAGACACAG 60
QY 61 TTCTCATTTCTTTTACATCTTGGCAACGCTGTGTATCTGTGTGTGTGTGTGTGTGT 120
Db 61 TTCTCATTTCTTTTACATCTTGGCAACGCTGTGTATCTGTGTGTGTGTGTGTGTGT 120
QY 121 CGCTGCTGGGCGCCCTGAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 121 CGCTGCTGGGCGCCCTGAGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 181 GTGGCAGAGTATCATCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 181 GTGGCAGAGTATCATCTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 241 CGGCGCAGT 300
Db 241 CGGCGCAGT 300
QY 301 GTGACCTGT 360
Db 301 GTGACCTGT 360
QY 361 AACTCAG 420
Db 361 AACTCAG 420

QY 421 GCCGTACTTCGCTGCGCCCTCATCTTACAGAGGCGACAGAGGCCCCCAGCGCGG 480
DB 421 GCGGTACTTCGCTGCGCCCTCATCTTACAGAGGCGACAGAGGCCCCCAGCGCGG 480
QY 481 CGCGCCCAAGTGCAGAGCTCAACAGAGAGGCTGTGATCTCTGAGCTTCAGATCTGATCT 540
DB 481 CGCGCCCAAGTGCAGAGCTCAACAGAGAGGCTGTGATCTCTGAGCTTCAGATCTGATCT 540
QY 541 TTCTTTGCTCTCTGCTCATCATGATCTTGTCTTACCTGCGCATCTAAGTATGCGCAA 600
DB 541 TTCTTTGCTCTCTGCTCATCATGATCTTGTCTTACCTGCGCATCTAAGTATGCGCAA 600
QY 601 CGCAGCAACCGCAGAGAGTCCCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
DB 601 CGCAGCAACCGCAGAGAGTCCCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 CCCCGACCCGACATGAGTGGGCTTTTGGCTCAGCCAACTGCGAGCCCTGCTGTG 720
DB 661 CCCCGACCCGACATGAGTGGGCTTTTGGCTCAGCCAACTGCGAGCCCTGCTGTG 720
QY 721 GCTTCTGCGCAGAGAGTTCACGACACTCTGAGTCCAGTGGGAGAGAGAGAGAGAGAG 780
DB 721 GCTTCTGCGCAGAGAGTTCACGACACTCTGAGTCCAGTGGGAGAGAGAGAGAGAGAG 780
QY 781 ACCCTTGAAGATATTGGGAGCCCGGCGCTTGGCAGCCAGTTGGGCTTCCCACTCA 840
DB 781 ACCCTTGAAGATATTGGGAGCCCGGCGCTTGGCAGCCAGTTGGGCTTCCCACTCA 840
QY 841 GGCCAGGAGCCAGAGAGAGGAGTGTGTGGGAGTCTCCAGAGATGAAGCTGA----- 894
DB 841 GGCCAGGAGCCAGAGAGAGGAGTGTGTGGGAGTCTCCAGAGATGAAGCTGAAGAGAG 900
QY 895 ---GAGAGAGAGAGAGAGAGAGAGAGTGTGAACCCCAAGGAGTGTCTTCCGCC 951
DB 901 GAGAGAGAGAGAGAGAGAGAGAGAGTGTGAACCCCAAGGAGTGTCTTCCGCC 960
QY 952 TCAGCTTGCAGAGCCCGCGCTGCGACAGCAGAGGCTCCCGGAGTGGCGGCGCTAAGT 1011
DB 961 TCAGCTTGCAGAGCCCGCGCTGCGACAGCAGAGGCTCCCGGAGTGGCGGCGCTAAGT 1020
QY 1012 GGCCAGGAGTCTCTGAGGAGAGGAGGAGTGTGATAGTGGGAGTGTGGCGTTCAGAG 1071
DB 1021 GGCCAGGAGTCTCTGAGGAGAGGAGGAGTGTGATAGTGGGAGTGTGGCGTTCAGAG 1080
QY 1072 GCGCAGCTGAGCCCGGAGAGAGCGCTTCACTTGTGCTGTGTGTGATTTGCGTTT 1131
DB 1081 GCGCAGCTGAGCCCGGAGAGAGCGCTTCACTTGTGCTGTGTGTGATTTGCGTTT 1140
QY 1132 GTGCTGTGCTGAGTCCCGCTTCTTCTTCAAGCTAAGCGCTGGGCGGCGATTCGCGAGAG 1191
DB 1141 GTGCTGTGCTGAGTCCCGCTTCTTCTTCAAGCTAAGCGCTGGGCGGCGATTCGCGAGAG 1200
QY 1192 TGCAAGTGTGCGCAGTGGCTCTTCCAGTCTTCTTGTGATCGGCTAATGCAAGAGCTCA 1251
DB 1201 TGCAAGTGTGCGCAGTGGCTCTTCCAGTCTTCTTGTGATCGGCTAATGCAAGAGCTCA 1260
QY 1252 CTGAACCTCTGTATCTAATCAATCTTCAACAGAGAGTTCGCGCGTGTCTTCCGAGAGATC 1311
DB 1261 CTGAACCTCTGTATCTAATCAATCTTCAACAGAGAGTTCGCGCGTGTCTTCCGAGAGATC 1320
QY 1312 CTGTGCGCGCGCTGAGAGCCAGAGCGGCGTGTGA 1344
DB 1321 CTGTGCGCGCGCTGAGAGCCAGAGCGGCGTGTGA 1353

RESULT 7
ACAS6583
ID ACAS6583 standard; cDNA, 2072 BP.
ACAS6583;
AC
XX
XX
DT 06-JUN-2003 (first entry)

XX DE Human signalling pathway polynucleotide probe SEQ ID NO 1181.
XX KW Human; probe; ss; array element; Parkinson's disease;
XX KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
XX KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX OS Homo sapiens.
XX PN US6500938-B1.
XX PD 31-DEC-2002.
XX PR 30-JAN-1998; 98US-0016434.
XX PR 30-JAN-1998; 98US-0016434.
XX (INCY-) INCYTE GENOMICS INC.
XX Au-Young J, Seilhamer JI;
XX WPI; 2003-352189/33.
XX PT Combination of polynucleotide probes, useful as array elements in a
XX PT microarray for monitoring the expression of a number of target
XX PT polynucleotides -
PS Claim 1; SEQ ID NO 1181; 65pp; English.
XX CC The invention relates to a combination which, comprises a number of
XX CC polynucleotide probes comprising a sequence selected from one of the 1490
XX CC sequences mentioned in the specification. The combination is useful as an
XX CC array element in a microarray for monitoring the expression of a number
XX CC of target polynucleotides. The microarray is particularly useful in the
XX CC diagnosis and treatment of cancer and immunopathology and neuropathology.
XX CC The microarray is useful in diagnostic and treatment regimens, drug
XX CC discovery and development, toxicological and carcinogenicity studies,
XX CC forensic and pharmacogenomics. The microarray is also useful for
XX CC monitoring progression of diseases and for developing sophisticated
XX CC profiles for the effects of currently available therapeutic drugs. The
XX CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
XX CC and genomic fragments and in research and diagnostic applications. The
XX CC array can detect changes in expression in a large number of genes coding
XX CC for different signalling pathway populations which can be used to diagnose
XX CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
XX CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
XX CC and Parkinson's disease. The present sequence represents a polynucleotide
XX CC probe of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format directly from USPTO
XX CC at sequence.uspto.gov/sequence.html?docid=06500938B1.
SQ Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 other;
Query Match 98.3%; Score 1321.8; DB 25; Length 2072;
Best Local Similarity 99.2%; Pred. No. 2,4e-254;
Matches 1342; Conservative 0; Mismatches 2; Indels 9; Gaps 1;
QY 1 ATGAGCACCAAGAGACCCCTTACTCGTGCAGAGCCACAGCGGCGGCGGCGGCGGCGG 60
DB 413 ATGAGCACCAAGAGACCCCTTACTCGTGCAGAGCCACAGCGGCGGCGGCGGCGGCGGCGG 472
QY 61 TTCTCATTTCTTTTACATCTTTCGAGAGAGCTGTGATCTTCTGCTGTGATGACGAGC 120
DB 473 TTCTCATTTCTTTTACATCTTTCGAGAGAGCTGTGATCTTCTGCTGTGATGACGAGC 532
QY 121 CGCTGCTGCGCGCCCTTCAAGAACCTGTTCTGTGTGTGCTGTGCGCGCGCGCATCTCTG 180
DB 533 CGCTGCTGCGCGCCCTTCAAGAACCTGTTCTGTGTGTGCTGTGCGCGCGCGCATCTCTG 592
QY 181 GTGCGCAGGCTCATCATCTCTTCTGCTGTGCGCAGAGAGTGTGCTGTGATCTTCTG 240
DB 593 GTGCGCAGGCTCATCATCTCTTCTGCTGTGCGCAGAGAGTGTGCTGTGATCTTCTG 652

| | | | |
|----|------|--|------|
| OY | 241 | GGGCGCAGTGGTGGAGGTGACCTGGGCGCTCGACAGTGTCTTTGTGACCTGCTGCATC | 300 |
| Db | 653 | CGGCGCAGTGGTGGAGGTGACCTGGGCGCTCGACAGTGTCTTTGTGACCTGCTGCATC | 712 |
| OY | 301 | GTGCACCTGTGGCCATCAGCTGTGACCGCTACTGTGGGCGTGTGACCGCGCGCTGTGAGTAC | 360 |
| Db | 713 | GTGCACCTGTGGCCATCAGCTGTGACCGCTACTGTGGGCGTGTGACCGCGCGCTGTGAGTAC | 772 |
| OY | 361 | AACTTCAAAGCGCACCCCGCGCGCATCAAGTGCATATCTTCACTGTGTGCTCATGTGCC | 420 |
| Db | 773 | AACTTCAAAGCGCACCCCGCGCGCATCAAGTGCATATCTTCACTGTGTGCTCATGTGCC | 832 |
| OY | 421 | GCCGTGATCTGGCTGCGCCCGCTCATCTACAAAGGGCGACCAAGGGCCCCCAAGCGCGGG | 480 |
| Db | 833 | GCCGTGATCTGGCTGCGCCCGCTCATCTACAAAGGGCGACCAAGGGCCCCCAAGCGCGGG | 892 |
| OY | 481 | CGCCCCCAGTGCAGACTCAACCAAGAGGCGTGTATCTGTGGCTCCAGCATCGGATCT | 540 |
| Db | 893 | CGCCCCCAGTGCAGACTCAACCAAGAGGCGTGTATCTGTGGCTCCAGCATCGGATCT | 952 |
| OY | 541 | TTCTTTGCTCCTTGTCTATCATGATCTTGTCTTACCTGTGCATTACTGATCGCCAA | 600 |
| Db | 953 | TTCTTTGCTCCTTGTCTATCATGATCTTGTCTTACCTGTGCATTACTGATCGCCAA | 1012 |
| OY | 601 | CGCAGCAACCGCAGAGTTCACAGGGCCAAAGGGGGGGCTTGGCAGAGGTGATCCAGCAG | 660 |
| Db | 1013 | CGCAGCAACCGCAGAGTTCACAGGGCCAAAGGGGGGGCTTGGCAGAGGTGATCCAGCAG | 1072 |
| OY | 661 | CCCCGACCCGACCAATGTGTGGGCTTTGGCTTCAGCCAACTGTGCCAGCCCTGGCCTGTGTG | 720 |
| Db | 1073 | CCCCGACCCGACCAATGTGTGGGCTTTGGCTTCAGCCAACTGTGCCAGCCCTGGCCTGTGTG | 1132 |
| OY | 721 | GCTTCTGCGCAGAGAGTCAACGACACTCGAAGTCACTGTGGAGAACAGAGAGGGGAG | 780 |
| Db | 1133 | GCTTCTGCGCAGAGAGTCAACGACACTCGAAGTCACTGTGGAGAACAGAGAGGGGAG | 1192 |
| OY | 781 | ACCCTTGAAGATCTGGGACCCCGGGCTTGGCCACCAGTGTGGGCTGCCCTTCCCACTCA | 840 |
| Db | 1193 | ACCCTTGAAGATCTGGGACCCCGGGCTTGGCCACCAGTGTGGGCTGCCCTTCCCACTCA | 1252 |
| OY | 841 | GGCCAGGGCCAGAAAGAGGGGTGTTGTGGGCGATCTCCAGAGAGTGAAGCTGAA----- | 894 |
| Db | 1253 | GGCCAGGGCCAGAAAGAGGGGTGTTGTGGGCGATCTCCAGAGAGTGAAGCTGAA----- | 1312 |
| OY | 895 | ---GAGAGAGAGAGAGAGAGAGAGTGTGAACCCAGAGGACAGTGCCTCGCGCC | 951 |
| Db | 1313 | GAAAGAGAGAGAGAGAGAGAGAGTGTGAACCCAGAGGACAGTGCCTCGCGCC | 1372 |
| OY | 952 | TCAAGTTGCAAGCCCCCGCTGAGCAGCACAGGGCTCCCGAGTGTGGCACCCTTACGT | 1011 |
| Db | 1373 | TCAAGTTGCAAGCCCCCGCTGAGCAGCACAGGGCTCCCGAGTGTGGCACCCTTACGT | 1432 |
| OY | 1012 | GGCCAGGTGCTCTGTGGCAGAGGGCGTGGGTCTATAGTGTGGCAGTGGTGCCTGTGAAGG | 1071 |
| Db | 1433 | GGCCAGGTGCTCTGTGGCAGAGGGCGTGGGTCTATAGTGTGGCAGTGGTGCCTGTGAAGG | 1492 |
| OY | 1072 | GCGCAGCTGACCCCGGAGAACCGCTTCACTTTCGTGTGCGTGTGTGTATTTGGGCTTTT | 1131 |
| Db | 1493 | GCGCAGCTGACCCCGGAGAACCGCTTCACTTTCGTGTGCGTGTGTGTATTTGGGCGTTTTT | 1552 |
| OY | 1132 | GTGCTGTGCTGTTCCTCCCTTCTTCTTTCAGTACACAGCTGTGGCGGCATCTGCGCGAAGAC | 1191 |
| Db | 1553 | GTGCTGTGCTGTTCCTCCCTTCTTCTTTCAGTACACAGCTGTGGCGGCATCTGCGCGAAGAC | 1612 |
| OY | 1192 | TGCAAGGTGCCCATGTGCCTTTCAGTCTTCTTCTTGTGGATCGGCTACTGTCAACAGCTCA | 1251 |
| Db | 1613 | TGCAAGGTGCCCATGTGCCTTTCAGTCTTCTTCTTGTGGATCGGCTACTGTCAACAGCTCA | 1672 |
| OY | 1252 | CTGAACCTGTATTCTACACATCTTCAACCAAGACTTCGCGCGTGTCTTCCGAGAGATC | 1311 |
| Db | 1673 | CTGAACCTGTATTCTACACATCTTCAACCAAGACTTCGCGCGTGTCTTCCGAGAGATC | 1732 |

0Y 1312 CTGTCGCGCCGCTGAGACCAAGCGGCTGTGA 1344
 |||||
 DB 1733 CTGTCCCGCCCGTGTGACCAAGCGGCTGTGA 1765
 |||||
 RESULT 8
 ID AB242624
 AC AB242624 standard; DNA; 3274 BP.
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.
 XX
 XX Homo sapiens.
 OS
 PN MO200261087-A2.
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US50107.
 PR 19-DEC-2000; 2000US-257144P.
 XX
 (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA
 PI Burner GC, Roush CL, Brown JP;
 DR MPI: 2003-046718/04.
 XX P-PSDB; ABP81780.
 PT
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX
 XX Disclosure; Fig 1; 523pp; English.
 XX
 XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP93619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be

CC used in immunosays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.

XX Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 other;

Query Match 98.3%; Score 1321.8; DB 25; Length 3274;

Best Local Similarity 99.2%; Pred. No. 2.6e-254; Indels 9; Gaps 1;

Matches 1342; Conservative 0; Mismatches 2; Indels 9; Gaps 1;

1 ATGAGACCAACAGAGACCCCTACTCCGTGACAGGCAAGGCGCAATAGCGCGCCATCACC 60
1 ATGAGACCAACAGAGACCCCTACTCCGTGACAGGCAAGGCGCAATAGCGCGCCATCACC 60
61 TTCTCATTTCTTTTACATCTTGGGCAAGCTTGGTCTATCTGCTGGTGTGACAGC 120
61 TTCTCATTTCTTTTACATCTTGGGCAAGCTTGGTCTATCTGCTGGTGTGACAGC 120
121 CGCTCGCTGCGCGCCCTCAGAAACCTGTTCTGCTGCTGCTGCGCCGCGCAATCTG 180
121 CGCTCGCTGCGCGCCCTCAGAAACCTGTTCTGCTGCTGCTGCGCCGCGCAATCTG 180
181 GTGGCCACGCTCATCATCCCTTTCTCGTGGCCAAAGAGCTGCTGCTGCTGCTGCTG 240
181 GTGGCCACGCTCATCATCCCTTTCTCGTGGCCAAAGAGCTGCTGCTGCTGCTGCTG 240
241 CGGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
241 CGGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
301 GTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
301 GTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
361 AACTCAAGCGCACCCCGCGCGCATCATAGTGCATCTCTGCTGCTGCTGCTGCTGCTG 420
361 AACTCAAGCGCACCCCGCGCGCATCATAGTGCATCTCTGCTGCTGCTGCTGCTGCTG 420
421 GCGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
421 GCGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
481 CGCCCGACAGTGCATCATCAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
481 CGCCCGACAGTGCATCATCAACAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
541 TTCTTTGCTCTTCTGCTCATCATATCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
541 TTCTTTGCTCTTCTGCTCATCATATCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
601 CGGAGCAACCGGACAGGCTCCAGAGGCGCAAGGCGCGCTGCGAGGAGTCCAGAGAG 660
601 CGGAGCAACCGGACAGGCTCCAGAGGCGCAAGGCGCGCTGCGAGGAGTCCAGAGAG 660
661 CCCGACCCGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
661 CCCGACCCGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
721 GCTTCTGCTCAGAGAGTCAACGAGACTCGAAGTCTGAGGAGAGAGAGAGAGAGAGAG 780
721 GCTTCTGCTCAGAGAGTCAACGAGACTCGAAGTCTGAGGAGAGAGAGAGAGAGAGAG 780
781 ACCCTGAAAGTATCTGGGAGCCCGGCTTGCACACCAATTTGGGCTTCCCAACTCA 840
781 ACCCTGAAAGTATCTGGGAGCCCGGCTTGCACACCAATTTGGGCTTCCCAACTCA 840
841 GGCACGAGGCTCAG 900
841 GGCACGAGGCTCAG 900
895 ---GAG 951
895 ---GAG 951
901 GAAAG 960
901 GAAAG 960

952 TCAGCTTGCAGCCGCCCGCTGACAGCCACAGGAGCTCCCGGCTGCTGCTGCTGCTGCT 1011
961 TCAGCTTGCAGCCGCCCGCTGACAGCCACAGGAGCTCCCGGCTGCTGCTGCTGCTGCT 1020
1012 GGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
1021 GGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
1072 GGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131
1081 GGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
1132 GGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
1141 GGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
1192 TGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1251
1201 TGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
1252 TGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311
1261 TGCAGAGTCTCTTGGGACAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
1312 CTGTGCGCGCGCTGAGCCAGAGCGGCTGCTG 1344
1321 CTGTGCGCGCGCTGAGCCAGAGCGGCTGCTG 1353

RESULT 9

AA014151
ID AA014151 standard; DNA; 2064 BP.

AA014151;

06-JUN-1992 (first entry)

Human alpha 2 beta adrenergic receptor gene.

Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.

Homo sapiens.

Key Location/Qualifiers
288..1752
CDS /*tag= a

US5053337-A.

01-OCT-1991.

30-OCT-1989; 89US-0428856.

30-OCT-1989; 89US-0428856.

(NEUR-) NEUROGENETIC CORP.

Weinshank RL, Hartig PR;

WPI; 1991-310087/42.

P-PSDB; AAR14149.

Isolated DNA encoding human adrenergic receptor - for detecting
nucleic acids encoding alpha, 2-beta adrenergic receptor, for
screening drugs.

Claim 1; Fig 2; 15pp; English.

Clone NGC-alpha2beta was isolated from a human spleen genomic
library by screening with a fragment of the human 5-HT1A receptor
gene. The gene can be used to express recombinant receptor protein
which can be used to produce antibodies for inhibition of receptor

CC function.
 XX Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 other;
 SQ
 Query Match 96.9%; Score 1302.6; DB 12; Length 2064;
 Best Local Similarity 98.3%; Pred. No. 1.ee-250;
 Matches 1330; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 1 ATGAGCACCAAGAGACCCCTACTCCGTGACAGCCACAGCGGCATATGAGGGGCGCATAC 60
 DB 399 ATGAGCACCAAGAGACCCCTACTCCGTGACAGCCACAGCGGCATATGAGGGGCGCATAC 458
 QY 61 TTCCTATCTCTTTACCATCTTCCGACAGCTCTGTCTATCTGCTGATGATGACAGC 120
 DB 459 TTCCTATCTCTTTACCATCTTCCGACAGCTCTGTCTATCTGCTGATGATGACAGC 518
 QY 121 CGCTCGCTGCGCGCCCTCAAGACCTGTTCTGTGTCTGCTGCGCGCGCGCATCTG 180
 DB 519 CGCTCGCTGCGCGCCCTCAAGACCTGTTCTGTGTCTGCTGCGCGCGCGCATCTG 578
 QY 181 GTGSCACAGCTCATACATCCCTTCTGCTGSCCAAGAGCTGCTGCTATCTGATCTTC 240
 DB 579 GTGSCACAGCTCATACATCCCTTCTGCTGSCCAAGAGCTGCTGCTATCTGATCTTC 638
 QY 241 CGGCGACAGTGTGCGAGGTGTACTGCGCTGACAGCTGCTTCTGACCTGTCATC 300
 DB 639 CGGCGACAGTGTGCGAGGTGTACTGCGCTGACAGCTGCTTCTGACCTGTCATC 698
 QY 301 GTGACCTGTGCGCCATCAGCTTGAACCGCTACTGCGCGCTGAGCGCGCTGAGTAC 360
 DB 699 GTGACCTGTGCGCCATCAGCTTGAACCGCTACTGCGCGCTGAGCGCGCTGAGTAC 758
 QY 361 AACTCCAGGCGACCCCGCGCCGATCAAGTGCATCTCTCTGTGTGCTCATGCGC 420
 DB 759 AACTCCAGGCGACCCCGCGCCGATCAAGTGCATCTCTCTGTGTGCTCATGCGC 818
 QY 421 GCGGTATCTGCTGCGCGCCCTCATCTCAAGAGCGACAGAGGCGCGCGCGCG 480
 DB 819 GCGGTATCTGCTGCGCGCCCTCATCTCAAGAGCGACAGAGGCGCGCGCGCG 878
 QY 481 GCGCCCAAGTGCAGCTCAACAGAGGCGCTGTATCTCTGCGCTTCCAGCATGATCT 540
 DB 879 GCGCCCAAGTGCAGCTCAACAGAGGCGCTGTATCTCTGCGCTTCCAGCATGATCT 928
 QY 541 TTCTTTGCTCTGCTGCTCATCATGATCTCTGTCTACTGCGCATCTTACATGCGCAA 600
 DB 939 TTCTTTGCTCTGCTGCTCATCATGATCTCTGTCTACTGCGCATCTTACATGCGCAA 998
 QY 601 CGGACCAACCGAGAGGTCCAGAGGCGCAAGAGGCGCGCTGAGGATGATCAAGCAG 660
 DB 999 CGGACCAACCGAGAGGTCCAGAGGCGCAAGAGGCGCGCTGAGGATGATCAAGCAG 1058
 QY 661 CCCCGACCCGACCATGCTGAGGCTTTGCTGCTCAAGCCAACTGCGAGCCCTCTGTG 720
 DB 1059 CCCCGACCCGACCATGCTGAGGCTTTGCTGCTCAAGCCAACTGCGAGCCCTCTGTG 1118
 QY 721 GCTTCTGCGAGAGGTCAACGACACTGCAAGTCTCACTGTGGAGAAAGAGAGGGAG 780
 DB 1119 GCTTCTGCGAGAGGTCAACGACACTGCAAGTCTCACTGTGGAGAAAGAGAGGGAG 1178
 QY 781 ACCCTGAGAGTACTGAGGACCCGCGGCTTGGCAACCCAGTTGGGCTGCTTCCCACTCA 840
 DB 1179 ACCCTGAGAGTACTGAGGACCCGCGGCTTGGCAACCCAGTTGGGCTGCTTCCCACTCA 1238
 QY 841 GGGCAGGCGCAGAGAGGCTGTTTGTGTGGCACTTCTCAAGAGATGAGCTGAA----- 894
 DB 1239 GGGCAGGCGCAGAGAGGCTGTTTGTGTGGCACTTCTCAAGAGATGAGCTGAAAGAGAG 1298
 QY 895 ---GAGAGAGAGAGAGAGAGAGTGTAAACCCAGGCACTGCGAGTCTCGGCGC 951
 DB 1299 GAGAGAGAGAGAGAGAGAGTGTGTAAACCCAGGCACTGCGAGTCTCGGCGC 1358
 QY 952 TCAGCTTGAGCGCCCGCGCTGAGCAGCCACAGAGGCTCCGAGGTGCTGCGCACCTTACGT 1011

DB 1359 TCAGCTTGAGCGCCCGCGCTGAGCAGCCACAGAGGCTCCGAGTGTGCGCACCTTACGT 1418
 QY 1012 GGGCAGGCTGCTCTGAGCAGAGGCGCTGCGCTGCTATGAGTGGAGAGTGGCGCTCCAGAG 1071
 DB 1419 GGGCAGGCTGCTCTGAGCAGAGGCGCTGCGCTGCTATGAGTGGAGAGTGGCGCTCCAGAG 1478
 QY 1072 GGGCAGGCTGACCCGAGAGAGAGCGCTTCACTTCTGCTGAGCTGCTGCTATGAGCGTTT 1131
 DB 1479 GGGCAGGCTGACCCGAGAGAGAGCGCTTCACTTCTGCTGAGCTGCTGCTATGAGCGTTT 1538
 QY 1132 GTGCTGTGCTGTTCCCTTCTTCTTCACTGACAGCTGAGCGCCATCTGCGAGAGAC 1191
 DB 1539 GTGCTGTGCTGTTCCCTTCTTCTTCACTGACAGCTGAGCGCCATCTGCGAGAGAC 1598
 QY 1192 TGCAGAGTGGCCATGAGCGCTTCTTCACTTCTTCTGATGAGCTATGACAGCTCA 1251
 DB 1599 TGCAGAGTGGCCATGAGCGCTTCTTCACTTCTTCTGATGAGCTATGACAGCTCA 1658
 QY 1252 CTGACCCCTGTATCTTACACATCTTCAACAGAGACTTCCGCGCTTCCGAGAGATC 1311
 DB 1659 CTGACCCCTGTATCTTACACATCTTCAACAGAGACTTCCGCGCTTCCGAGAGATC 1718
 QY 1312 CTGTGCGCGCCGCTGAGCCAGAGCGCGCTGTGA 1344
 DB 1719 CTGTGCGCGCCGCTGAGCCAGAGCGCGCTGTGA 1751

RESULT 10
 AAT59499
 ID AAT59499 standard; DNA; 2064 BP.
 XX
 AC AAT59499;
 DT 25-MAR-2003 (updated)
 DT 06-MAY-1997 (first entry)
 XX
 DE Human alpha-2b adrenergic receptor genomic DNA clone.
 XX
 KW Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
 KW epinephrine; signal transduction; neurotransmitter; ligand; se.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 288..1751
 FT /*tag= a
 XX
 PN US595880-A.
 XX
 PD 21-JUN-1997.
 XX
 PF 22-OCT-1992; 92US-0965040.
 XX
 PR 30-OCT-1989; 89US-0428856.
 PR 20-MAY-1991; 91US-0707604.
 PR 22-OCT-1992; 92US-0965040.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 PI Hartig PR, Weinschank RL;
 XX
 DR WPI, 1997-107576/10.
 DR P-PSDB; AAW11804.
 XX
 PT Assay for alpha-2b adrenergic receptor ligands - using membranes of
 PT cells expressing recombinant receptor
 XX
 PS Disclosure, Fig 2A-B, 16pp; English.
 XX
 CC A genomic DNA clone (AAT59499) codes for human alpha-2b adrenergic
 CC receptor (AAW11804), a member of the rhodopsin-like signal transducer
 CC family. It was isolated from a human spleen genomic library in the

